



DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIITITKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120  
 DB 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120  
 QY 121 TLTNHLKQDASAEVERLERRENOVLSVRIDAKKYPSSODSSAAAPOLLIVL 172  
 DB 121 TLTNHLKQDASAEVERLERRENOVLSVRIDAKKYPSSODSSAAAPOLLIVL 172

RESULT 2  
 AAM65771  
 ID AAM65771 standard; protein; 180 AA.

AC AAM65771;  
 DT 20-NOV-1998 (first entry)

DE Protein recognised by anti-human HML.24 antibody.

XX Cytotoxic antibody; anti-human HML.24; lymphocytic tumours;  
 KM pre-B lymphoma; Burkitt's lymphoma; T-cell tumour; B-cell tumour.

XX Homo sapiens.

OS MO9835698-A1.

PN 20-AUG-1998.

PF 12-FEB-1998; 98WO-JP000568.

PR 12-FEB-1997; 97JP-00041410.

PI (CHUS) CHUGAI SEIYAKU KK.

PI Kohshihara Y, Yoshimura Y;

DR MPI; 1998-456869/39.

DR N-PSDB; AAV07579.

PT Treatment of lymphocytic tumours using cytotoxic antibody - binding to  
 specific antigen such as HML.24 and effective against T-cell tumours and  
 B-cell tumours other than myeloma.

PS Claim 1; Page 44-45; 82pp; Japanese.

XX The protein having the amino acid sequence below is bound specifically by  
 CC a cytotoxic antibody which can be used in the treatment of lymphocytic  
 CC tumours, including T-cell tumours and B-cell tumours other than myeloma.  
 CC The antibody is preferably monoclonal and has AACC or CDC type  
 CC cytotoxicity. It may be chimeric or humanised, and preferably contains a  
 CC human antibody constant region C gamma (such as C gamma 1 or C gamma 3).  
 CC A preferred antibody is an anti-human HML.24 antibody or an antibody  
 CC which binds to an epitope recognising anti-human HML.24 antibody. The  
 CC cytotoxic antibody is useful in the treatment of lymphocytic tumours such  
 CC as acute or chronic B lymphocytic leukaemia, pre-B lymphoma, Burkitt's  
 CC lymphoma, or acute or chronic T lymphocytic leukaemia

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIITITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIITITKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120  
 DB 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120

QY 121 TLTNHLKQDASAEVERLERRENOVLSVRIDAKKYPSSODSSAAAPOLLIVL 172  
 DB 121 TLTNHLKQDASAEVERLERRENOVLSVRIDAKKYPSSODSSAAAPOLLIVL 172

RESULT 3  
 AAM62207  
 ID AAM62207 standard; protein; 180 AA.

AC AAM62207;

DT 21-SEP-1998 (first entry)

DE Humanised anti-HML.24 antibody polypeptide.

XX Mouse; human; humanised; anti-HML.24 antibody; myeloma; FR; CDR;  
 KM framework region; complementarity determining region; antigenicity.

OS Synthetic.

OS Mus sp.

OS Homo sapiens.

PN WO9814580-A1.

PD 09-APR-1998.

PF 03-OCT-1997; 97WO-JP003553.

PR 04-OCT-1996; 96JP-00264756.

PI (CHUS) CHUGAI SEIYAKU KK.

PI Ono K, Ohtomo T, Tsuchiya M, Yoshimura Y, Kohshihara Y, Kosaka M;

DR MPI; 1998-286421/25.

DR N-PSDB; AAV39359.

PT Humanised anti-HML.24 antibody - for treatment of myeloma.

PS Claim 81; Page 151-153; 210pp; Japanese.

XX A humanised anti-HML.24 antibody has been developed which comprises human  
 CC L and H chain C regions, and L and/or H chain V regions containing  
 CC material originating in mouse anti-HML.24 antibody. The V regions contain  
 CC framework (FR) regions of human origin and complementarity determining  
 CC regions (CDR) of mouse origin, leading to a reshaped humanised antibody.  
 CC The C regions are human Ck (L-chain) and human C gamma (especially C  
 CC gamma 1) (H-chain). The FR regions of the L chain V region are derived  
 CC from human subtype HSG1 (e.g. from human antibody RE1) and the FR regions  
 CC of the H chain V region are derived from human subtype HSG1 (e.g. FR1-3  
 CC from human antibody Hg3 and FR4 from human antibody Hg6). The present  
 CC sequence represents an antibody polypeptide from the present invention.  
 CC The antibodies are used for the treatment of myeloma, especially by  
 CC injection, intravenously, intramuscularly or subcutaneously. The  
 CC antibodies are used at 0.01-1000 (especially 5-1000 mg/kg body weight.  
 CC The humanised antibody has low antigenicity and is therefore effective  
 CC therapeutically in humans

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIITITKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPPLIITITKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120  
 DB 61 MECRNVTHTLLOQELTEAOKGFODVEAQAATCNHTWALMASLDAEKAQOKVEELEGEI 120

OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 4

AA02576  
 ID AA02576 standard; protein; 180 AA.

AA02576;

16-JUL-1999 (first entry)

HML.24 antigenic protein.

Reconstituted human antibody; peptide antigen HML.24; framework region; complementary determining region; CDR; anti-HML.24 antibody; myeloma; humanised antibody.

Homo sapiens.

WO9918212-A1.

15-APR-1999.

02-OCT-1998; 98WO-JP004469.

03-OCT-1997; 97JP-00271726.

(CHUS ) CHUGAI SEIYAKU KK.

Tsuchiya M;

WPI; 1999-277273/23.

N-PSDB; AAX59485.

Reconstituted human antibody useful in the treatment of myeloma.

Disclosure; Page 131-133; 256pp; Japanese.

The specification describes a reconstituted human antibody recognising the peptide antigen HML.24. This human antibody contains natural human framework regions modified by amino acid substitutions to provide homogeneity with a previously designed framework region (which may arise from a human or non-human source); and complementary determining regions (CDR) derived from a non-human anti-HML.24 antibody. The reconstituted antibody is useful in the treatment of diseases in which the surface antigen HML.24 is implicated such as myeloma. The present sequence represents HML.24 antigenic protein

Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVLGVPPIIFITIKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVLGVPPIIFITIKANSEACRDGLRAV 60  
 OY 61 MECRVNTHLQOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELEGEI 120  
 DB 61 MECRVNTHLQOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELEGEI 120  
 OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 5  
 ID AA02576 standard; protein; 180 AA.

AC AA02576;  
 XX 25-OCT-1999 (first entry)

AA02576;

16-JUL-1999 (first entry)

HML.24 antigenic protein.

Homo sapiens.

WO9943703-A1.

02-SEP-1999.

25-FEB-1999; 99WO-JP000885.

25-FEB-1998; 98JP-00060613.

(CHUS ) CHUGAI SEIYAKU KK.

Ozaki Y, Koishihara Y;

WPI; 1999-518836/43.

N-PSDB; AAZ10917.

Immunosay of anti-HML.24 antibody or soluble HML.24 antigen, useful for diagnosis of immune disorders and cancer.

Example 3; Fig 14-15; 138pp; Japanese.  
 This sequence represents a human soluble HML.24 antigenic protein. The invention relates to an immunochemical assay of anti-HML.24 antibody by use of a soluble HML.24 antigenic protein, or an immunochemical assay of the soluble antigen by use of the antibody. The immunoassay of the HML.24 antigen or antibody is useful for diagnosis of immune disorders and cancer, for monitoring of anti-HML.24 antibody immunotherapy, and for assay of the antibody or antigen for investigative purposes, in biological samples such as blood, serum, urine, milk, synovial fluid or microorganism culture media. The method is sensitive down to 500 pg/ml antibody

Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVLGVPPIIFITIKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVLGVPPIIFITIKANSEACRDGLRAV 60  
 OY 61 MECRVNTHLQOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELEGEI 120  
 DB 61 MECRVNTHLQOELTEAOKGFQDVEAQAATCNHTVMALMASIDAEKAOQKVEELEGEI 120  
 OY 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172  
 DB 121 TLLNHLKODASAEVERLRRENOVL SVRIADKKYYPSSODSSAAAPOLLITVL 172

RESULT 6  
 ID AA02576 standard; protein; 180 AA.

AA02576;

22-NOV-1999 (first entry)

Human HML.24 antigenic protein.

Antigenic protein; HML.24; splice variant; promoter; antineoplastic; antitumor; bone marrow; tumour cell; drug development; treatment;

KM myeloma, rheumatoid arthritis; human.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9943803-A1.  
 XX  
 PD 02-SEP-1999.  
 XX  
 PF 25-FEB-1999; 99WO-JP000884.  
 XX  
 PR 25-FEB-1998; 98JP-00060617.  
 XX  
 PR 24-MAR-1998; 98JP-00093883.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Ohtomo T, Tsuchiya M, Koishihara Y, Kosaka M;  
 XX  
 DR WPI, 1999-550869/46.  
 XX  
 DR N-PSDB; AA209726.  
 XX  
 PT Genomic DNA encoding Hm1.24 antigen protein as well as splicing variants,  
 PT useful e.g. in development of drugs for treating myeloma and rheumatoid  
 PT arthritis.  
 XX  
 PS Example 1; Fig 1-2; 83pp; Japanese.  
 XX  
 CC This invention describes a novel human antigenic protein, Hm1.24, its  
 CC encoding nucleic acid, splice variants and promoter region. The products  
 CC of the invention have antirheumatic and antiarthritic activity. The DNA  
 CC of the invention is isolated from bone marrow tumour cells, which can be  
 CC used to study the expression of Hm1.24 antigen, promoter activity of its  
 CC promoter region, and in development of drugs in treating e.g. myeloma and  
 CC rheumatoid arthritis. This sequence represents the human Hm1.24 antigenic  
 CC protein described in the invention  
 XX  
 SQ Sequence 180 AA;  
 XX  
 Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASTSYDYCRVPMEDGDRCKLLGIGIIVLIIIVLGVPILITFKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDRCKLLGIGIIVLIIIVLGVPILITFKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAKAGOKKVELEGEI 120  
 DB 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAKAGOKKVELEGEI 120  
 QY 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 DB 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 XX  
 RESULT 7  
 AAY05484  
 ID AAY05484 standard; protein; 180 AA.  
 XX  
 AC AAY05484;  
 XX  
 DT 07-JUL-1999 (first entry)  
 XX  
 DE Potentiator for antibody against lymphoid tumour.  
 XX  
 KW Antibody potentiator; lymphoid tumour; lymphoma; cytotoxic antibody;  
 KW multiple myeloma; acute B-lymphocytoma; chronic B-lymphocytoma;  
 KW pre-B lymphoma; Burkitt's lymphoma; acute T-lymphocytoma; therapy;  
 KW chronic T-lymphocytoma; PNTL.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9918997-A1.  
 XX

PD 22-APR-1999.  
 XX  
 PF 14-OCT-1998; 98WO-JP004645.  
 XX  
 PR 14-OCT-1997; 97JP-00280759.  
 XX  
 PR 05-AUG-1998; 98JP-00222024.  
 XX  
 PA (CHUS ) CHUGAI SEIYAKU KK.  
 XX  
 PI Kosaka M, Koishihara Y;  
 XX  
 DR WPI, 1999-277447/23.  
 XX  
 DR N-PSDB; AAX36561.  
 XX  
 PT Potentiation of antibody treatment of lymphoma with biological response  
 PT modifier.  
 XX  
 PS Claim 1; Page 37-38; 62pp; Japanese.  
 XX  
 CC This sequence represents a potentiator for an antibody against lymphoid  
 CC tumour. The invention relates to a method for the treatment of lymphoma,  
 CC in which a cytotoxic antibody is potentiated by administration of a  
 CC biological response modifier. The method can be used for treatment of  
 CC lymphomas and multiple myelomas which are resistant to conventional  
 CC treatment, such as acute B-lymphocytoma, chronic B-lymphocytoma, pre-B  
 CC lymphoma, Burkitt's lymphoma, acute T-lymphocytoma, chronic T-  
 CC lymphocytoma, and PNTL  
 XX  
 SQ Sequence 180 AA;  
 XX  
 Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MASTSYDYCRVPMEDGDRCKLLGIGIIVLIIIVLGVPILITFKANSEACRDLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDRCKLLGIGIIVLIIIVLGVPILITFKANSEACRDLRAV 60  
 QY 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAKAGOKKVELEGEI 120  
 DB 61 MECRNVTHTLQOELTEAOKGFQDVEAQAATCNHTVMALMASLDAKAGOKKVELEGEI 120  
 QY 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 DB 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSQDSSAAAPQLLIIVL 172  
 XX  
 RESULT 8  
 AAY07250  
 ID AAY07250 standard; protein; 180 AA.  
 XX  
 AC AAY07250;  
 XX  
 DT 06-JUL-1999 (first entry)  
 XX  
 DE BST-2 protein.  
 XX  
 KW Mouse; BST-2; monoclonal antibody; RS38; myeloma; cytotoxic activity.  
 KW Mus sp.  
 XX  
 PN JP11092399-A.  
 XX  
 PD 06-APR-1999.  
 XX  
 PF 24-SEP-1997; 97JP-00274960.  
 XX  
 PR 24-SEP-1997; 97JP-00274960.  
 XX  
 PA (CHUS ) CHUGAI PHARM CO LTD.  
 XX  
 DR WPI, 1999-283503/24.  
 XX  
 DR N-PSDB; AAX29996.  
 XX

XX An agent for treating myeloma -includes an antibody and has cytotoxic  
 PT activity.  
 XX

PS Claim 1; Page 10; 13pp; Japanese.

CC This sequence represents the mouse B27-2 protein which is used to raise  
 CC antibodies, especially the monoclonal antibody RS38. The antibody can be  
 CC used in compositions to treat myelomas when the antibody is associated  
 CC with a cytotoxic activity

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 2; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDGLRAV 60  
 QY 61 MECRVVTHLLOELTEAOKGFQDVBAQAATCNHTVMALMASIDAKKAGOKKVEELBEGI 120  
 DB 61 MECRVVTHLLOELTEAOKGFQDVBAQAATCNHTVMALMASIDAKKAGOKKVEELBEGI 120  
 QY 121 TILNHKLDASAEVERLRERNOVLSVRIDAKKYPSODSSAAAPOLLIVL 172  
 DB 121 TILNHKLDASAEVERLRERNOVLSVRIDAKKYPSODSSAAAPOLLIVL 172

RESULT 9  
 AAY53273

ID AAY53273 standard; protein; 180 AA.

XX AAY53273;

XX 21-JUN-2000 (first entry)

DE Human HML.24 antigen protein sequence SEQ ID NO:2.

XX Human; HML.24 antigen protein; detection; plasmocytoma; multiple myeloma;  
 KW plasmocytic leukaemia; extramedullary plasmocytoma;  
 KW multiple plasmocytoma; asymptomatic myeloma.

XX Homo sapiens.

XX WO200017395-A1.

XX 30-MAR-2000.

XX 20-AUG-1999; 99WO-JP004502.

XX 18-SEP-1998; 98JP-00264593.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Kawai S, Koshihara Y, Kosaka M;

XX WPI; 2000-283616/24.

XX N-PSDB; AAA13654.

PT Detection or measurement of plasmocytomas, applicable for early diagnosis  
 PT of e.g. multiple myeloma and plasmocytic leukemia, using a polynucleotide  
 PT which is expressed specifically or strongly in plasmocytomas.

XX Disclosure; Page 15-16; 20pp; Japanese.

XX A method has been developed for detecting or measuring plasmocytomas in a  
 CC sample at an early stage of disease development. The method comprises  
 CC amplifying a polynucleotide which is expressed specifically or strongly  
 CC in plasmocytomas before quantifying the amplification product by  
 CC comparing with results obtained with a control sample. The method is for  
 CC detecting or measuring plasmocytomas, applicable for early diagnosis of

CC e.g. multiple myeloma, plasmocytic leukaemia, isolated plasmocytoma,  
 CC extramedullary plasmocytoma, multiple plasmocytoma obtained from smoking  
 CC or asymptomatic myeloma. The present sequence represents human HML.24  
 CC antigen protein, which is expressed in plasmocytomas and so can be used  
 CC in the method of the invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 3; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDGLRAV 60  
 DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDGLRAV 60  
 QY 61 MECRVVTHLLOELTEAOKGFQDVBAQAATCNHTVMALMASIDAKKAGOKKVEELBEGI 120  
 DB 61 MECRVVTHLLOELTEAOKGFQDVBAQAATCNHTVMALMASIDAKKAGOKKVEELBEGI 120  
 QY 121 TILNHKLDASAEVERLRERNOVLSVRIDAKKYPSODSSAAAPOLLIVL 172  
 DB 121 TILNHKLDASAEVERLRERNOVLSVRIDAKKYPSODSSAAAPOLLIVL 172

RESULT 10  
 AAB70697

ID AAB70697 standard; protein; 180 AA.

XX AAB70697;

XX 18-MAY-2001 (first entry)

DE Human HML.24 antigen protein sequence SEQ ID NO:2.

XX Human; HML.24 antigen expression potentiator; HML.24 protein antigen;  
 KW myeloma; interferon alpha; interferon gamma; IFN-alpha; IFN-gamma;  
 KW interferon regulatory factor 2; IRF-2; cytostatic; cytotoxic antibody;  
 KW multiple myeloma.

XX Homo sapiens.

XX WO200113940-A1.

XX 01-MAR-2001.

XX 22-AUG-2000; 2000WO-JP005617.

XX 23-AUG-1999; 99JP-00236007.

XX 16-FEB-2000; 2000JP-00038689.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Kosaka M, Ozaki S, Wakahara Y;

XX WPI; 2001-202921/20.

XX N-PSDB; AAF74792.

PT HML.24 antigen expression potentiating agent containing interferon alpha  
 PT or gamma or IRF-2 for treatment of myeloma.

XX Claim 1; Page 55-56; 72pp; Japanese.

XX The present invention describes an agent for potentiating the expression  
 CC of HML.24 antigen in myeloma cells. The agent contains as an active  
 CC component interferon (IFN) alpha or gamma, or interferon regulatory  
 CC factor 2 (IRF-2), or a compound promoting the expression of IRF-2. Also  
 CC described are: (1) drug compositions for the treatment of myeloma which  
 CC contain the HML.24 antigen expression potentiating agent together with a  
 CC cytotoxic antibody binding to HML.24 antigen; (2) screening compounds for  
 CC their activity in potentiating the expression of IRF-2; and (3) kits for  
 CC the treatment of myeloma using the HML.24 antigen expression potentiating  
 CC agent and a cytotoxic antibody. The agent has cytostatic activity and can

CC be used for the treatment of myeloma, especially of multiple myeloma. The  
CC present sequence represents the human HMI.24 protein antigen

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDGLRAV 60  
DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDGLRAV 60  
QY 61 MECRVNTHLLOQELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120  
DB 61 MECRVNTHLLOQELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120  
QY 121 TTIHNKLODASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172  
DB 121 TTIHNKLODASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

RESULT 11  
ABBS0295  
ID ABB50295 standard; protein; 180 AA.

XX ABB50295;

DT 08-FEB-2002 (first entry)

XX Bone marrow stromal antigen (BST-2) ovarian tumour marker protein, #80.

XX Ovarian tumour marker gene; human; overexpression; upregulation;  
KM epithelial tumour; cancer; diagnosis; prognosis; disease monitoring;  
KM identification; serous cystadenoma; borderline serous tumour;  
KM serous cystadenocarcinoma; mucinous cystadenocarcinoma;  
KM mucinous cystadenoma; borderline mucinous tumour; endometrioid carcinoma;  
KM undifferentiated carcinoma; clear cell adenocarcinoma; cystadenofibroma;  
KM adenofibroma; Brenner tumour; serial analysis of gene expression; SAGE;  
KM immune response pathway; cell proliferation regulation; protein folding;  
KM membrane localised; secreted; therapeutic target; cytostatic;  
KM gene therapy; vaccine.

XX Homo sapiens.

XX WO200175177-A2.

XX 11-OCT-2001.

XX 03-APR-2001; 2001WO-US010947.

XX 03-APR-2000; 2000US-0194336P.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Morin PJ, Sherman-Baust CA, Pizer ES, Hough CD;

XX WPI; 2001-626450/72.

DR N-PSDB; ABA83121.

XX Detecting and identifying ovarian tumor, identifying increased risk for  
PT developing ovarian cancer, and determining effectiveness of ovarian  
PT cancer treatment, by measuring expression level of ovarian tumor marker  
PT gene.

XX Claim 23; Page 124; 140pp; English.

XX The invention relates to methods for diagnosing and prognosing ovarian  
CC tumours in an individual via the detection and measurement of the  
CC expression of ovarian tumour marker genes (ABA83081-ABA83122, ABA83180,  
CC ABA83182 and ABA83184) or segments thereof (ABA83123-ABA83169, ABA83179,  
CC ABA83181 and ABA83183). The methods of the invention are useful for  
CC detecting an ovarian tumour in a patient, for identifying an individual

CC at increased risk for developing ovarian cancer, in prognostic tests for  
CC assessing the relative severity of ovarian cancer, in tests for  
CC monitoring a patient in remission from ovarian cancer and in tests for  
CC monitoring disease status in a patient being treated for ovarian cancer.  
CC The methods can additionally be used to identify a particular tumour as  
CC being an ovarian tumour (i.e., an epithelial ovarian tumour selected from  
CC serous cystadenoma, borderline serous tumour, serous cystadenocarcinoma,  
CC mucinous cystadenoma, endometrioid carcinoma, undifferentiated carcinoma,  
CC cystadenocarcinoma, cystadenofibroma, adenofibroma and Brenner  
CC tumour. The ovarian tumour marker genes of the invention were identified  
CC using SAGE (serial analysis of gene expression) and were found to be  
CC overexpressed in a broad variety of ovarian epithelial tumour cells  
CC relative to normal ovarian epithelial cells. The marker genes are  
CC implicated in immune response pathways, in the regulation of cell  
CC proliferation and in protein folding, and many of these are membrane-  
CC localised or secreted. In addition to their use as diagnostic and  
CC prognostic markers, the ovarian tumour marker genes or their encoded  
CC proteins may be used as therapeutic targets for the treatment and  
CC prevention of ovarian cancer. Sequences ABB50257-ABB50299 represent  
CC proteins encoded by ovarian tumour marker genes of the invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDGLRAV 60  
DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVLGVPLIIFITKANSEACRDGLRAV 60  
QY 61 MECRVNTHLLOQELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120  
DB 61 MECRVNTHLLOQELTEAKGQFQDVEAQAATCNHTVMALMSLDKAKQGGKVEELGEI 120  
QY 121 TTIHNKLODASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172  
DB 121 TTIHNKLODASAEVRLRRENOVLSVRIADKKYPPSSODSSAAPOLLIVL 172

RESULT 12

ABBS3492  
ID ABB83492 standard; protein; 180 AA.

XX ABB83492;

DT 04-OCT-2002 (first entry)

XX Human Bone Marrow Stromal Antigen 2, BST2.

KM Human; bone marrow stromal antigen 2; BST2; cytostatic; antirheumatic;  
KM antigen; lymphoma; cancer; multiple myeloma; rheumatism.

XX Homo sapiens.

XX WO200257316-A1.

XX 25-JUL-2002.

XX 26-DEC-2001; 2001WO-JP011493.

XX 28-DEC-2000; 2000JP-00403245.

XX (KIRI ) KIRIN BEER KK.

XX Tahara T;

XX WPI; 2002-557847/59.

DR N-PSDB; ABB8330.

PT Monoclonal antibody binding to human cell surface antigen BST2 for  
PT treatment and diagnosis of cancer rheumatism and lymphoma.

XX Claim 7; Fig 5; 49pp; Japanese.

PS The present invention relates to a monoclonal antibody, which can bind to  
 CC human cell surface antigen B8T2 (Bone Marrow Stromal Antigen 2), and is  
 CC capable of internalizing into the cell. A complex, comprising the  
 CC monoclonal antibody and a therapeutic drug, can be used for treatment of  
 CC lymphoma, cancer, multiple myeloma and rheumatism. The antibody complex  
 CC effectively introduces the bound drug to the cell interior. The present  
 CC sequence is the protein sequence for human B8T2

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
 DB 1 MASTSYDCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
 QY 61 MECRVNTHLLQOELTEAQGFQDVEAQAATCNHTVMALMASIDAEKAGQCKVELEGSI 120  
 DB 61 MECRVNTHLLQOELTEAQGFQDVEAQAATCNHTVMALMASIDAEKAGQCKVELEGSI 120  
 QY 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSOSSSAAAPQLLIVL 172  
 DB 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSOSSSAAAPQLLIVL 172

RESULT 13

ABP53548  
 ID ABP53548 standard; protein; 180 AA.

AC ABP53548;

DT 14-DEC-2002 (first entry)

DE Human HML.24 protein antigen SEQ ID NO:2.

XX Human; HML.24 protein antigen; tumour, hematopoietic; interferon alpha;  
 KM Interferon gamma; IRF-2; interferon-regulatory factor-2; cytostatic;  
 KW Leukaemia; lymphoma; myeloma.

XX Homo sapiens.

OS WO200264159-A1.

PN 22-AUG-2002.

XX 06-FEB-2002; 2002WO-JP000989.

XX 07-FEB-2001; 2001JP-00031492.

XX (CHUS) CHUGAI SEIYAKU KK.

XX Kosaka M, Ozaki S, Wakahara Y;

XX WPI: 2002-682719/73.

DR N-PSDB; ABQ82202.

PT Remedies for tumors in hematopoietic organs e.g. leukemia, lymphoma or  
 PT myeloma, containing HML.24 antigen expression inducers or potentiators in  
 PT tumor cells e.g. interferon approximately or approximately, or IRF-2  
 PT and anti-HML.24 antibody.

XX Claim 1; Page 73; 93pp; Japanese.

XX The present invention describes expression potentiators (I) or inducers  
 CC of the human HML.24 protein antigen 180 amino acid residue sequence (II)  
 CC in tumour cells of hematopoietic organs containing interferon alpha or  
 CC gamma or IRF-2 (interferon-regulatory factor-2) protein as an active  
 CC ingredient. Also described are remedies or drug compositions for tumours

CC in hematopoietic organs containing interferon alpha or gamma or IRF-2  
 CC protein, and an antibody binding specifically to HML.24, or their various  
 CC combinations. (II) have cytostatic activities. The remedies can be used  
 CC for treating tumors in hematopoietic organs e.g. leukemia, lymphoma or  
 CC myeloma. The present sequence represents the human HML.24 protein antigen  
 CC from the present invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
 DB 1 MASTSYDCRVPMEDGDKRCKLLIGILVLLIIVILGVPILITITKANSEACRDLRAV 60  
 QY 61 MECRVNTHLLQOELTEAQGFQDVEAQAATCNHTVMALMASIDAEKAGQCKVELEGSI 120  
 DB 61 MECRVNTHLLQOELTEAQGFQDVEAQAATCNHTVMALMASIDAEKAGQCKVELEGSI 120  
 QY 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSOSSSAAAPQLLIVL 172  
 DB 121 TTLNKHLDQASAEVERLRRENOVLSVRIADKKYPSOSSSAAAPQLLIVL 172

RESULT 14

ABP61469  
 ID ABP61469 standard; protein; 180 AA.

AC ABP61469;

DT 30-SEP-2002 (first entry)

DE Human NF-kB activating protein SEQ ID NO 91.

XX Human; NF-kB; nuclear factor kappa B; mouse; antiinflammatory;  
 KM immunomodulator; cytostatic; antiinfective; osteopathic; nootropic;  
 KW neuroprotective; anti-HIV; autoimmune disease; cancer; infection;  
 KW bone disease; AIDS; neurodegenerative disease; ischaemic disorder.

XX Homo sapiens.

OS WO200253737-A1.

PN 11-JUL-2002.

XX 25-DEC-2001; 2001WO-JP011389.

XX 28-DEC-2000; 2000JP-00402288.

XX 26-MAR-2001; 2001JP-00088912.

XX 24-AUG-2001; 2001JP-00254018.

XX (ASAH) ASAH KASEI KOGYO KK.

XX Matsuda A, Honda G, Muramatsu S, Nagano Y;

XX WPI: 2002-583617/62.

DR N-PSDB; ABQ91957.

PT NF-approximatelykB activating gene and expressed protein, applicable in  
 PT diagnosis and screening inhibitors or promoters to control excessive  
 PT activation or inhibition for treating e.g. inflammations, autoimmune  
 PT diseases and cancer.

XX Claim 1; Page 413-414; 841pp; Japanese.

XX The invention relates to a purified protein (I), comprising one of 90  
 CC fully defined sequences (ABP61424-ABP61513) or a protein based on any of  
 CC the sequences but with some amino acids deleted, substituted or added and  
 CC with a NF-kB (nuclear factor kappa B) activating effect. The protein and  
 CC encoding gene (ABQ91912-ABQ92001) are useful in diagnosis and screening  
 CC inhibitors or promoters to control excessive activation or inhibition and

CC For treating e.g. inflammations, autoimmune diseases, cancers,  
CC infections, bone diseases, AIDS, neurodegenerative diseases or ischaemic  
CC disorders  
XX  
SQ Sequence 180 AA;

Query Match. 100.0%; Score 854; DB 5; Length 180;  
Best Local Similarity 100.0%; Pred. No. 6.9e-75;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
DB 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
QY 61 MECRNVTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELBGEI 120  
DB 61 MECRNVTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELBGEI 120  
QY 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPPSSQDSSAAAPQLLIIVL 172  
DB 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPPSSQDSSAAAPQLLIIVL 172

# RESULT 15

AAM52356  
ID AAM52356 standard; protein; 180 AA.

AC AAM52356;

DT 25-JAN-2002 (first entry)

DE Human Hm1.24 antigen which is expressed on cell membranes.

KW Hm1.24 antigen; antibody; extracellular domain; immunoassay; human.

XX Homo sapiens.

XX WO200177362-A1.

XX 18-OCT-2001.

XX 05-APR-2001; 2001WO-JP002964.

XX 06-APR-2000; 2000JP-00105423.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Kinoshita Y, Iehikawa Y;

XX WPI; 2002-010919/01.

XX N-PSDB; ABA01226.

XX Preparation of soluble Hm1.24 antigen extracellular domain, useful for

XX immunoassay of Hm1.24 antigen.

XX Dielosure; Fig 6; 96pp; Japanese.

XX The present invention relates to a method for preparing soluble Hm1.24

XX antigen extracellular domain. The method comprises culturing animal cells

XX transformed by an expression vector carrying Erialpha (undefined).

XX promoter and Hm1.24 antigen gene. The invention can be used for

XX immunoassay of Hm1.24 antigen. The method is more sensitive to

XX conventional enzyme linked immunoassay (ELISA) methods. The

XX present sequence was used to illustrate the present invention

XX Sequence 180 AA;

Query Match 100.0%; Score 854; DB 5; Length 180;

Best Local Similarity 100.0%; Pred. No. 6.9e-75;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60

DB 1 MASTSYDYCRVPMEDGDKCKLLIGILVLLIIVILGVPLIIFTIKANSEACRDGLRAV 60  
QY 61 MECRNVTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELBGEI 120  
DB 61 MECRNVTHTLLOQELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELBGEI 120  
QY 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPPSSQDSSAAAPQLLIIVL 172  
DB 121 TTLNHLQDASAEVERLRRENOVLSYRIADKYYPPSSQDSSAAAPQLLIIVL 172

Search completed: December 29, 2004, 11:45:39  
Job time : 84 secs



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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 27 Seconds  
(without alignments)  
422.470 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854

Sequence: 1 MASTSYDYCRVPMEDGDKRC.....YTPSSQSSSAAPQLIVL 172

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PTCS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 854   | 100.0       | 180    | 2     | US-08-624-650-1    |
| 2          | 854   | 100.0       | 180    | 4     | US-09-818-648-1    |
| 3          | 854   | 100.0       | 180    | 4     | US-09-355-925-5    |
| 4          | 854   | 100.0       | 180    | 4     | US-09-787-3375-2   |
| 5          | 854   | 100.0       | 180    | 4     | US-09-622-166A-3   |
| 6          | 854   | 100.0       | 180    | 4     | US-09-269-921-129  |
| 7          | 490   | 57.4        | 156    | 4     | US-09-622-166A-20  |
| 8          | 99.5  | 11.7        | 270    | 2     | US-09-055-095-4    |
| 9          | 99.5  | 11.7        | 270    | 2     | US-08-809-494A-2   |
| 10         | 99.5  | 11.7        | 270    | 3     | US-09-352-302-2    |
| 11         | 99.5  | 11.7        | 273    | 2     | US-08-809-494A-4   |
| 12         | 99.5  | 11.7        | 273    | 3     | US-09-352-302-4    |
| 13         | 95.5  | 11.2        | 977    | 4     | US-09-010-147B-18  |
| 14         | 95    | 11.1        | 885    | 2     | US-08-533-306A-4   |
| 15         | 95    | 11.1        | 885    | 2     | US-08-742-923A-4   |
| 16         | 95    | 11.1        | 1857   | 4     | US-09-917-254-91   |
| 17         | 95    | 11.1        | 1937   | 4     | US-09-538-092-918  |
| 18         | 95    | 11.1        | 1972   | 4     | US-08-875-435B-4   |
| 19         | 95    | 11.1        | 1972   | 4     | US-09-538-092-1084 |
| 20         | 93    | 10.9        | 1972   | 4     | US-08-875-435B-3   |
| 21         | 92.5  | 10.8        | 210    | 2     | US-09-222-938A-67  |
| 22         | 92.5  | 10.8        | 292    | 2     | US-08-688-342-4    |
| 23         | 92.5  | 10.8        | 292    | 2     | US-09-113-788-4    |
| 24         | 92.5  | 10.8        | 292    | 2     | US-09-862-802A-12  |
| 25         | 92.5  | 10.8        | 392    | 4     | US-09-583-110-4374 |
| 26         | 92.5  | 10.8        | 534    | 4     | US-09-103-664A-2   |
| 27         | 92.5  | 10.8        | 1886   | 3     | US-08-938-105-3    |

|    |      |      |      |   |                      |                   |
|----|------|------|------|---|----------------------|-------------------|
| 28 | 92   | 10.8 | 165  | 4 | US-09-898-554-24     | Sequence 24, Appl |
| 29 | 90.5 | 10.6 | 1935 | 4 | US-09-538-092-916    | Sequence 916, App |
| 30 | 90.5 | 10.6 | 1939 | 4 | US-09-538-092-915    | Sequence 915, App |
| 31 | 89.5 | 10.5 | 316  | 3 | US-09-111-470-4      | Sequence 4, Appl  |
| 32 | 89.5 | 10.5 | 316  | 4 | US-09-862-802A-4     | Sequence 4, Appl  |
| 33 | 89   | 10.4 | 363  | 4 | US-09-898-554-20     | Sequence 20, Appl |
| 34 | 88.5 | 10.4 | 397  | 4 | US-09-252-991A-23027 | Sequence 23027, A |
| 35 | 88.5 | 10.4 | 1939 | 3 | US-09-310-187A-1     | Sequence 1, Appl  |
| 36 | 88.5 | 10.4 | 1939 | 4 | US-09-538-092-917    | Sequence 917, App |
| 37 | 88.5 | 10.4 | 1940 | 4 | US-09-538-092-901    | Sequence 901, App |
| 38 | 88   | 10.3 | 207  | 4 | US-09-898-554-26     | Sequence 26, Appl |
| 39 | 88   | 10.3 | 288  | 3 | US-08-312-949-4      | Sequence 4, Appl  |
| 40 | 88   | 10.3 | 288  | 3 | US-08-446-201-4      | Sequence 4, Appl  |
| 41 | 88   | 10.3 | 619  | 1 | US-08-465-746-2      | Sequence 2, Appl  |
| 42 | 88   | 10.3 | 619  | 1 | US-08-214-164-2      | Sequence 2, Appl  |
| 43 | 88   | 10.3 | 619  | 2 | US-08-467-852A-3     | Sequence 3, Appl  |
| 44 | 88   | 10.3 | 619  | 2 | US-08-246-836-2      | Sequence 2, Appl  |
| 45 | 88   | 10.3 | 619  | 2 | US-08-247-491A-3     | Sequence 3, Appl  |

## ALIGNMENTS

RESULT 1  
US-08-624-650-1  
; Sequence 1, Application US/08624650  
; Patent No. 5914252  
GENERAL INFORMATION:  
APPLICANT: HIRANO, TOSHIO  
APPLICANT: KAIISHO, TSUNEYASU  
TITLE OF INVENTION: MEMBERANE PROTEIN POLYPEPTIDE HAVING  
TITLE OF INVENTION: PER-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
ADDRESS: P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/624, 650  
FILING DATE: 22-MAY-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP94/01732  
FILING DATE: 14-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 5-281622  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-413-3000  
TELEFAX: 703-413-2220  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 180 amino acids  
TYPE: amino acid  
STRANDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-624-650-1  
Query Match 100.0%; Score 854; DB 2; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

QY 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

DB 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

QY 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

DB 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 2  
US-09-818-648-1

Sequence 1, Application US/09818648

Patent No. 6489126

GENERAL INFORMATION:

APPLICANT: HIRANO, TOSHIO

TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING

PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/818,648

FILING DATE: 28-Mar-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/624,650

FILING DATE: 22-May-1996

APPLICATION NUMBER: PCT/JP94/01732

FILING DATE: 14-Oct-1994

APPLICATION NUMBER: JP 5-281622

FILING DATE: 15-Oct-1993

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 7625-001-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-818-648-1

Query Match

Best Local Similarity 100.0%; Pred. No. 2.4e-84;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

QY 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

DB 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

QY 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

DB 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 3

US-09-355-925-5

Sequence 5, Application US/09355925

Patent No. 6503510

GENERAL INFORMATION:

APPLICANT: KOISHIBARA, YASUO

APPLICANT: YOSHIMURA, YASUSHI

TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS

FILE REFERENCE: 053466/0255

CURRENT APPLICATION NUMBER: US/09/355,925

PRIOR FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT/JP98/00568

PRIOR FILING DATE: 1998-02-12

PRIOR APPLICATION NUMBER: JP 9-41410

PRIOR FILING DATE: 1997-02-12

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 5

LENGTH: 180

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Amino acid sequence of Hm1.24 antigen

US-09-355-925-5

Query Match

Best Local Similarity 100.0%; DB 4; Length 180;

Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

DB 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVPLIIFITKANSEACRDLRAV 60

QY 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

DB 61 MCCRNVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKGKVEELGEI 120

QY 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

DB 121 TTLNHLQDASAEVERLRRENOVLSVRIADKKYYPSSODSSAAAPOLLIVL 172

RESULT 4

US-09-787-375-2

Sequence 2, Application US/09787375

Patent No. 6602663

GENERAL INFORMATION:

APPLICANT: KAMAI, SHIGETO

APPLICANT: KOISHIBARA, YASUO

TITLE OF INVENTION: METHOD FOR DETECTION OR MEASUREMENT OF PLASMACYTOMA CELLS

FILE REFERENCE: 053466/0301

CURRENT APPLICATION NUMBER: US/09/787,375

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: PCT/JP99/04502

PRIOR FILING DATE: 1999-08-20

PRIOR APPLICATION NUMBER: JP 10-264593

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 180

TYPE: PRT

ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of HM1.24 antibody protein  
US-09-787-315-2

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Db 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120

Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172

RESULT 5  
US-09-622-166a-3  
Sequence 3, Application US/09622166a  
Patent No. 6613546  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: KOSAKA, MASAOKI  
TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
FILE REFERENCE: 053466/0285  
CURRENT FILING DATE: US/09/622,166a  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/JP99/00884  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 10-60617  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 10-93883  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 3  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-622-166a-3

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Db 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120

Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172

RESULT 6  
US-09-269-921-129  
Sequence 129, Application US/09269921  
Patent No. 6699974  
GENERAL INFORMATION:  
APPLICANT: Ono, Koichiro

APPLICANT: Ohtomo, Toshihiko  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yoshimura, Yasushi  
APPLICANT: Koishihara, Yasuo  
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
FILE REFERENCE: 35029-20007.00  
CURRENT FILING DATE: US/09/269,921  
CURRENT FILING DATE: 1999-04-01  
EARLIER APPLICATION NUMBER: PCT/JP97/03553  
EARLIER FILING DATE: 1997-10-03  
EARLIER APPLICATION NUMBER: JP 8-264756  
EARLIER FILING DATE: 1996-10-04  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 129  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
US-09-269-921-129

Query Match 100.0%; Score 854; DB 4; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2.4e-84;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60  
Db 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

Qy 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120  
Db 61 MECRNVTLLQOELTEAOKGFQDVEAQAATCNHTYMAALMASLDAKAGOKKVEELGEI 120

Qy 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172  
Db 121 TTLNHNKLDASAEVERLRRENOVLSVRIADKKYPPSSQDSSSAAPQLLIIVL 172

RESULT 7  
US-09-622-166a-20  
Sequence 20, Application US/09622166a  
Patent No. 6613546  
GENERAL INFORMATION:  
APPLICANT: OHTOMO, TOSHIHIKO  
APPLICANT: TSUCHIYA, MASAYUKI  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: KOSAKA, MASAOKI  
TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
FILE REFERENCE: 053466/0285  
CURRENT FILING DATE: US/09/622,166a  
PRIOR FILING DATE: 2000-08-14  
PRIOR APPLICATION NUMBER: PCT/JP99/00884  
PRIOR FILING DATE: 1999-02-25  
PRIOR APPLICATION NUMBER: 10-60617  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 10-93883  
NUMBER OF SEQ ID NOS: 33  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 20  
LENGTH: 156  
TYPE: PRT  
ORGANISM: Mus sp.  
US-09-622-166a-20

Query Match 57.4%; Score 480; DB 4; Length 156;  
Best Local Similarity 85.6%; Pred. No. 4e-45;  
Matches 101; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

Qy 1 MASTSYDVCRVPMEDGDRCKLLGIGILVLLIIVLGVPLIIFITKANSEACRDLRAV 60

DB 1 MASTSDYCRVMEBDSCKLLIGLIVLIIIVLIPLIITIKANSEACRDLRAV 60  
QY 61 MECRNVTLLLOQLTEAOKGFQDVEAQAATCNHTMALASDAEKAQOKVBELEG 118  
DB 61 MECRNVTLLLOQLTEAOKGFQDVEAQAATCNHTYAR-KPGIKREN-RQOEVLPLQPG 116

## RESULT 8

US-09-055-095-4  
; Sequence 4, Application US/09055095  
; Patent No. 5945308  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Patterson, Chandra  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Sacher, Susan  
; TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Dr.  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/055,095  
; FILING DATE: Filed Herewith  
; CLASSIFICATION:  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER:  
; ATTORNEY/AGENT INFORMATION:  
; FILING DATE:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0500 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 1902982  
; US-09-055-095-4

Query Match 11.7%; Score 99.5; DB 2; Length 270;  
Best Local Similarity 25.9%; Pred. No. 0.013;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGLIVLIIIVLIPLIITIKANSEACRDLRAVMECRNVTHLLQOELTEAOKGFQ 82  
DB 40 VLCLGLVTVIILIIQLSGVSDLIKQO-----ANITH--QEDILEGQ----- 80  
QY 83 DVEAQAATCNHTYAR-MALASDAEKAQOKVBELEGITTLNHNKLODASAVERLRRENO 142  
DB 81 -----ILAQRRSEKS-AQESQKELKEMITFLAHKLDKSKKLMELHRQVL 124  
QY 143 VLSVRIADKKY--PSSQD 159  
DB 125 NLOEVLKEAANYSGPCPD 143

RESULT 9  
US-08-809-494A-2  
; Sequence 2, Application US/08809494A  
; Patent No. 5962260  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; APPLICANT: Masaki, Tomoo  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,494A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-321705  
; FILING DATE: 30-NOV-1994  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-214206  
; FILING DATE: 31-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REGISTRATION NUMBER: 24408  
; REFERENCE/DOCKET NUMBER: JG-YY-4363PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 818-9479  
; TELEFAX: 212 818-9479  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-809-494A-2

Query Match 11.7%; Score 99.5; DB 2; Length 270;  
Best Local Similarity 25.9%; Pred. No. 0.013;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LIGIGLIVLIIIVLIPLIITIKANSEACRDLRAVMECRNVTHLLQOELTEAOKGFQ 82  
DB 40 VLCLGLVTVIILIIQLSGVSDLIKQO-----ANITH--QEDILEGQ----- 80  
QY 83 DVEAQAATCNHTYAR-MALASDAEKAQOKVBELEGITTLNHNKLODASAVERLRRENO 142  
DB 81 -----ILAQRRSEKS-AQESQKELKEMITFLAHKLDKSKKLMELHRQVL 124  
QY 143 VLSVRIADKKY--PSSQD 159  
DB 125 NLOEVLKEAANYSGPCPD 143

RESULT 10  
US-09-352-302-2  
; Sequence 2, Application US/09352302  
; Patent No. 6197937  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; APPLICANT: Masaki, Tomoo  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlulay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/352,302  
FILING DATE: 12-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 270 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-352-302-2

Query Match 11.7%; Score 99.5; DB 3; Length 270;  
Best Local Similarity 25.9%; Pred. No. 0.013; Indels 37; Gaps 5;  
Matches 36; Conservative 25; Mismatches 41

QY 23 LLGIGILVLLIVIGVPLIIFTIKANSEACRDGLRAVMECHVTNHLQOELETKAQGFQ 82  
DB 40 VLCLGLVTVLLILQLSGLVSLIKKQ-----ANTH--QEDILEGQ----- 80

QY 83 DVEAQAATCNHTVMALMSLAERKAGQKVELEGEITTLNHLKQDASAEVERLRRENO 142  
DB 81 -----ILAQRSSEKS-AQESQKELKEMETLTAHKLDKSKKLMEHLRQNL 124

QY 143 VLSVRIADKXY--PSSQD 159  
DB 125 NLQEVLKEANVSGPCPD 143

RESULT 11  
US-08-809-494A-4  
Sequence 4, Application US/08809494A  
Patent No. 5962260  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified Low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlulay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,494A  
FILING DATE: 24-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-809-494A-4

Query Match 11.7%; Score 99.5; DB 2; Length 273;  
Best Local Similarity 25.9%; Pred. No. 0.014;  
Matches 36; Conservative 25; Mismatches 41; Indels 37; Gaps 5;

QY 23 LLGIGILVLLIVIGVPLIIFTIKANSEACRDGLRAVMECHVTNHLQOELETKAQGFQ 82  
DB 43 VLCLGLVTVLLILQLSGLVSLIKKQ-----ANTH--QEDILEGQ----- 83

QY 83 DVEAQAATCNHTVMALMSLAERKAGQKVELEGEITTLNHLKQDASAEVERLRRENO 142  
DB 84 -----ILAQRSSEKS-AQESQKELKEMETLTAHKLDKSKKLMEHLRQNL 127

QY 143 VLSVRIADKXY--PSSQD 159  
DB 128 NLQEVLKEANVSGPCPD 146

RESULT 12  
US-09-352-302-4  
Sequence 4, Application US/09352302  
Patent No. 6197937  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified Low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlulay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/352,302  
FILING DATE: 12-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:



Oy 104 -AEKAGQOKVEELEGITTLNHLKQDASAEVERLRRENQVLSVRIADKK 152  
 Db 275 TRQKLNVTSTKLRQLEERNSLQDQDEMEAKONLRIHISTINIQLSDSK 324

RESULT 15

US-08-742-923A-4  
 ; Sequence 4, Application US/08742923A  
 ; Patent No. 5869611  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Pu  
 ; APPLICANT: Collins, Francis S.  
 ; APPLICANT: Siciliano, Michael J.  
 ; APPLICANT: Claxton, David  
 ; TITLE OF INVENTION: Markers for Detection of Chromosome 16  
 ; NUMBER OF INVENTIONS: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.  
 ; STREET: P.O. Box 828  
 ; CITY: Bloomfield Hills  
 ; STATE: MI  
 ; COUNTRY: USA  
 ; ZIP: 48303  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/742,923A  
 ; FILING DATE: No. 5869611ember 1, 1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, Dean F.  
 ; REGISTRATION NUMBER: 36683  
 ; REFERENCE/DOCKET NUMBER: 2115-00869DVC  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 641-1600  
 ; TELEFAX: (810) 641-0270  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 885 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-742-923A-4

Query Match 11.1%; Score 95; DB 2; Length 885;  
 Best Local Similarity 24.5%; Pred. No. 0.21; Indels 10; Gaps 1;  
 Matches 27; Conservative 18; Mismatches 55;  
 Oy 53 CRDGLRAVMEGNTVTLQOELETEAOKGFQDVEAQAATCNHTVMAIMASLD----- 103  
 Db 215 CSDEKRAAEALNDKXKQNEVESVTGMLNEAEKAKIKAKDVASLSQLODQTELLQEE 274  
 Oy 104 -AEKAGQOKVEELEGITTLNHLKQDASAEVERLRRENQVLSVRIADKK 152  
 Db 275 TRQKLNVTSTKLRQLEERNSLQDQDEMEAKONLRIHISTINIQLSDSK 324

Search completed: December 29, 2004, 11:44:10  
 Job time : 28 secs

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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 589 Seconds

(without alignments)  
105.048 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854  
Sequence: 1 MASTSYDCRVPMEDGDKRC.....YFSSQSSSAAPQLITVL 172

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1599051 seqs, 359727711 residues

Total number of hits satisfying chosen parameters: 1599051

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*  
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10: /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*  
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15: /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 854   | 100.0       | 180    | 9  | US-09-828-217-1   |
| 2          | 854   | 100.0       | 180    | 9  | US-09-760-723-5   |
| 3          | 854   | 100.0       | 180    | 9  | US-09-355-925-5   |
| 4          | 854   | 100.0       | 180    | 9  | US-09-818-648-1   |
| 5          | 854   | 100.0       | 180    | 10 | US-09-269-921-129 |
| 6          | 854   | 100.0       | 180    | 10 | US-09-509-098-129 |
| 7          | 854   | 100.0       | 180    | 13 | US-10-114-893-46  |
| 8          | 854   | 100.0       | 180    | 14 | US-10-171-311-20  |
| 9          | 854   | 100.0       | 180    | 14 | US-10-315-125-5   |
| 10         | 854   | 100.0       | 180    | 14 | US-10-218-253-129 |
| 11         | 854   | 100.0       | 180    | 14 | US-10-024-298A-91 |
| 12         | 854   | 100.0       | 180    | 14 | US-10-042-211A-91 |
| 13         | 854   | 100.0       | 180    | 14 | US-10-428-085-5   |

|    |       |       |     |    |                      |                    |
|----|-------|-------|-----|----|----------------------|--------------------|
| 14 | 854   | 100.0 | 180 | 14 | US-10-423-007-3      | Sequence 3, Appli  |
| 15 | 854   | 100.0 | 180 | 15 | US-10-257-021-80     | Sequence 80, Appli |
| 16 | 854   | 100.0 | 180 | 15 | US-10-617-217A-91    | Sequence 91, Appli |
| 17 | 854   | 100.0 | 180 | 16 | US-10-474-714-2      | Sequence 2, Appli  |
| 18 | 854   | 100.0 | 180 | 16 | US-10-451-847A-2     | Sequence 2, Appli  |
| 19 | 854   | 100.0 | 180 | 16 | US-10-755-889-386    | Sequence 386, App  |
| 20 | 854   | 100.0 | 180 | 17 | US-10-024-298A-91    | Sequence 91, Appli |
| 21 | 854   | 100.0 | 180 | 17 | US-10-473-127-815    | Sequence 815, App  |
| 22 | 854   | 100.0 | 180 | 17 | US-10-473-127-816    | Sequence 816, App  |
| 23 | 854   | 100.0 | 180 | 17 | US-10-473-127-818    | Sequence 818, App  |
| 24 | 854   | 100.0 | 180 | 17 | US-10-473-127-820    | Sequence 820, App  |
| 25 | 854   | 100.0 | 180 | 17 | US-10-473-127-821    | Sequence 821, App  |
| 26 | 854   | 100.0 | 180 | 17 | US-10-473-127-823    | Sequence 823, App  |
| 27 | 854   | 100.0 | 180 | 17 | US-10-473-127-824    | Sequence 824, App  |
| 28 | 854   | 100.0 | 180 | 17 | US-10-473-127-828    | Sequence 828, App  |
| 29 | 854   | 100.0 | 180 | 17 | US-10-473-127-831    | Sequence 831, App  |
| 30 | 854   | 100.0 | 180 | 17 | US-10-473-127-832    | Sequence 832, App  |
| 31 | 854   | 100.0 | 180 | 17 | US-10-473-127-833    | Sequence 833, App  |
| 32 | 854   | 100.0 | 180 | 17 | US-10-473-127-834    | Sequence 834, App  |
| 33 | 854   | 100.0 | 180 | 17 | US-10-370-715B-238   | Sequence 238, App  |
| 34 | 854   | 100.0 | 193 | 14 | US-10-106-698-4721   | Sequence 4721, App |
| 35 | 854   | 100.0 | 193 | 17 | US-10-473-127-817    | Sequence 817, App  |
| 36 | 847   | 99.2  | 180 | 17 | US-10-473-127-822    | Sequence 822, App  |
| 37 | 824.5 | 96.5  | 197 | 17 | US-10-473-127-819    | Sequence 819, App  |
| 38 | 614.5 | 72.0  | 143 | 17 | US-10-473-127-826    | Sequence 826, App  |
| 39 | 614   | 71.9  | 132 | 17 | US-10-473-127-825    | Sequence 825, App  |
| 40 | 614   | 71.9  | 161 | 17 | US-10-473-127-829    | Sequence 829, App  |
| 41 | 579   | 67.8  | 126 | 17 | US-10-473-127-830    | Sequence 830, App  |
| 42 | 574.5 | 67.3  | 126 | 17 | US-10-473-127-827    | Sequence 827, App  |
| 43 | 524   | 61.4  | 148 | 15 | US-10-264-049-4164   | Sequence 4164, App |
| 44 | 490   | 57.4  | 156 | 14 | US-10-423-007-20     | Sequence 20, Appli |
| 45 | 454   | 53.2  | 91  | 15 | US-10-424-599-221303 | Sequence 221303,   |

## ALIGNMENTS

RESULT 1  
US-09-828-217-1  
Sequence 1, Application US/09828217  
Patent No. US20010051710A1  
GENERAL INFORMATION:  
APPLICANT: KAIRANO, TOSHIO  
KAISHO, TSUNEYASU  
TITLE OF INVENTION: MEMBRANE PROTEIN POLYPEPTIDE HAVING  
PRE-B CELL GROWTH-SUPPORTING ABILITY AND A GENE THEREOF  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
P.C.  
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400  
CITY: ARLINGTON  
STATE: VA  
COUNTRY: USA  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/828,217  
FILING DATE: 09-Apr-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/182,563  
FILING DATE: <Unknown>  
APPLICATION NUMBER: PCT/JP94/01732  
FILING DATE: 14-OCT-1994  
APPLICATION NUMBER: JP 5-281622  
FILING DATE: 15-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: OBLON, NORMAN F.



FILING DATE: 14-OCT-1994  
 APPLICATION NUMBER: JP 5-281622  
 FILING DATE: 15-OCT-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: OBLON, NORMAN F.  
 REGISTRATION NUMBER: 24,618  
 REFERENCE/DOCKET NUMBER: 7625-001-0 PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-413-3000  
 TELEFAX: 703-413-2220  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 180 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-818-648-1

Query Match 100.0%; Score 854; DB 9; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60  
 Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 5  
 US-09-269-921-129  
 Sequence 129, Application US/09269921  
 Publication No. US20030045691A1  
 GENERAL INFORMATION:  
 APPLICANT: Ono, Koichiro  
 APPLICANT: Ohtomo, Toshihiko  
 APPLICANT: Tsuchiya, Masayuki  
 APPLICANT: Yoshimura, Yasuo  
 APPLICANT: Koshimura, Yasuo  
 TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
 FILE REFERENCE: 35029-20007.00  
 CURRENT APPLICATION NUMBER: US/09/269,921  
 EARLIER FILING DATE: 1999-04-01  
 EARLIER APPLICATION NUMBER: PCT/JP97/03553  
 EARLIER FILING DATE: 1997-10-03  
 EARLIER APPLICATION NUMBER: JP 8-264756  
 NUMBER OF SEQ ID NOS: 137  
 SOFTWARE: Patent Ver. 2.0  
 SEQ ID NO 129  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence  
 OTHER INFORMATION: of HM 1.24 antigen  
 US-09-269-921-129

Query Match 100.0%; Score 854; DB 10; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60

Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 6  
 US-09-509-098-129  
 Sequence 129, Application US/09509098  
 Publication No. US20030103970A1  
 GENERAL INFORMATION:  
 APPLICANT: TSUCHIYA, MASAYUKI  
 TITLE OF INVENTION: NATURAL HUMANIZED ANTIBODY  
 FILE REFERENCE: 053466/0274  
 CURRENT APPLICATION NUMBER: US/09/509,098  
 CURRENT FILING DATE: 2000-03-22  
 PRIOR APPLICATION NUMBER: PCT/JP98/04469  
 PRIOR FILING DATE: 1998-10-02  
 PRIOR APPLICATION NUMBER: JP 9-271726  
 NUMBER OF SEQ ID NOS: 203  
 SOFTWARE: Patent Ver. 2.1  
 SEQ ID NO 129  
 LENGTH: 180  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: HM1.24 antigenic protein  
 US-09-509-098-129

Query Match 100.0%; Score 854; DB 10; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60  
 |||||  
 Db 1 MASTSYDYCRVPMEDGDRCKLLGIGILVLLIIVILGVPPLIIFTIKANSEACRDLRAV 60  
 Qy 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 |||||  
 Db 61 MECSNVTHLLOEELTEAKGFQDVEAQAATCNHTVMALMASIDAEKAGQKKVEELBEI 120  
 Qy 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172  
 |||||  
 Db 121 TTLNHNKLODASAEVERLRERNOVLSVRIADKKYYPSSODSSAAPOLLIVL 172

RESULT 7  
 US-10-114-893-46  
 Sequence 46, Application US/10114893  
 Publication No. US20020193567A1  
 GENERAL INFORMATION:  
 APPLICANT: Jacobs, Kenneth  
 APPLICANT: McCoy, John M.  
 APPLICANT: Lavallie, Edward R.  
 APPLICANT: Collins-Racie, Lisa A.  
 APPLICANT: Evans, Cheryl  
 APPLICANT: Merberg, David  
 APPLICANT: Treacy, Maurice  
 APPLICANT: Bowman, Michael R.  
 APPLICANT: Spaulding, Vikki  
 APPLICANT: Carlin-Duckett, McKeough  
 APPLICANT: Kelleher, Kerry S.  
 APPLICANT: Genetics Institute, Inc.  
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM  
 FILE REFERENCE: GI 6000-10A  
 CURRENT APPLICATION NUMBER: US/10/114,893  
 CURRENT FILING DATE: 2002-04-02  
 EARLIER APPLICATION NUMBER: 09/413,232

EARLIER FILING DATE: 1999-10-06  
NUMBER OF SEQ ID NOS: 321  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 46  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-114-893-46

Query Match 100.0%; Score 854; DB 13; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
QY 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

RESULT 8  
US-10-171-311-20

Sequence 20, Application US/10171311  
Publication No. US20030087270A1  
GENERAL INFORMATION:  
APPLICANT: Schlegel, Robert  
APPLICANT: Chen, Yan  
APPLICANT: Zhao, Xumei  
APPLICANT: Monahan, John  
APPLICANT: Kamatkar, Shubhangi  
APPLICANT: Glatt, Karen  
APPLICANT: Gannavarapu, Manjula  
APPLICANT: Hoersch, Sebastian  
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
FILE REFERENCE: MRI-035  
CURRENT APPLICATION NUMBER: US/10/171,311  
CURRENT FILING DATE: 2002-06-12  
PRIOR APPLICATION NUMBER: US 60/298,159  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,155  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/335,936  
PRIOR FILING DATE: 2001-11-14  
NUMBER OF SEQ ID NOS: 238  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 20  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-171-311-20

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
QY 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

DB 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

RESULT 9  
US-10-315-125-5

Sequence 5, Application US/10315125  
Publication No. US20030113334A1  
GENERAL INFORMATION:  
APPLICANT: KOISHIHARA, YASUO  
APPLICANT: YOSHIMURA, YASUSHI  
TITLE OF INVENTION: THERAPEUTIC AGENT FOR LYMPHATIC TUMORS  
FILE REFERENCE: 053466/0255  
CURRENT APPLICATION NUMBER: US/10/315,125  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US/09/355,925  
PRIOR FILING DATE: 1997-02-12  
PRIOR APPLICATION NUMBER: PCT/J998/00568  
PRIOR FILING DATE: 1998-02-12  
PRIOR APPLICATION NUMBER: JP 9-41410  
PRIOR FILING DATE: 1997-02-12  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 5  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
OTHER INFORMATION: Amino acid sequence of Hm1.24 antigen  
US-10-315-125-5

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
DB 1 MASTSYDYCRVPMEDGDRCKLLIGILVLLIIVLGPPLIIFITKANSEACRDLRAV 60  
QY 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
DB 61 MECRVVTHLLOELTEAOKGFODVEAQAATCNHTWALMASIDAEKAGOKKVEELGEI 120  
QY 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172  
DB 121 TTLNKLQDASAEVERLRRENOVLSVRIADKKYPSODSSSAAPOLLIVL 172

RESULT 10  
US-10-218-253-129

Sequence 129, Application US/10218253  
Publication No. US20030129185A1  
GENERAL INFORMATION:  
APPLICANT: Ono, Koichiro  
APPLICANT: Ohtomo, Toshiniko  
APPLICANT: Tsuchiya, Masayuki  
APPLICANT: Yoshimura, Yasuaki  
APPLICANT: Koishihara, Yasuo  
TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY  
FILE REFERENCE: 35029-2007.00  
CURRENT APPLICATION NUMBER: US/10/218,253  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US/09/269,921  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: PCT/J997/03553  
PRIOR FILING DATE: 1997-10-03  
PRIOR APPLICATION NUMBER: JP 8-264756  
PRIOR FILING DATE: 1996-10-04  
NUMBER OF SEQ ID NOS: 137  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 129  
LENGTH: 180  
TYPE: PRT  
ORGANISM: Artificial sequence

Query Match 100.0%; Score 854; DB 14; Length 180;  
Best Local Similarity 100.0%; Pred. No. 2e-74;  
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence
OTHER INFORMATION: of HM 1.24 antigen
US-10-218-253-129

```

```

Query Match      100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60
Db 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60

Qy 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120
Db 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120

Qy 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172

```

```

RESULT 11
US-10-024-298A-91
Sequence 91, Application US/10024298A
Publication No. US20030143540A1
GENERAL INFORMATION:
APPLICANT: ASAMI KASEI KABUSHIKI KAISHA
APPLICANT: AKIO MATSUDA
APPLICANT: Goichi HONDA
APPLICANT: Shuji MURAMATSU
APPLICANT: Yukiko NAGANO
TITLE OF INVENTION: NF-K B Activating Gene
FILE REFERENCE: 1254-0191P
CURRENT APPLICATION NUMBER: US/10/024,298A
CURRENT FILING DATE: 2003-04-08
PRIOR APPLICATION NUMBER: 60/314,385
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/278,641
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP254018/2001
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: JP008912/2001
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP402288/2000
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-024-298A-91

```

```

Query Match      100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60
Db 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60

Qy 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120
Db 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120

Qy 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172

```

```

RESULT 12
US-10-042-211A-91
Sequence 91, Application US/10042211A
Publication No. US20030170719A1
GENERAL INFORMATION:
APPLICANT: MATSUDA, AKIO et al.
TITLE OF INVENTION: NFkB Activating Gene
FILE REFERENCE: 1254-0192P
CURRENT APPLICATION NUMBER: US/10/042,211A
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: JP 2000-402288
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: JP 2001-088912
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2001-254018
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/258,315
PRIOR FILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 60/278,640
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 60/314,385
PRIOR FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 91
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-042-211A-91

```

```

Query Match      100.0%; Score 854; DB 14; Length 180;
Best Local Similarity 100.0%; Pred. No. 2e-74;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60
Db 1 MASTSYDYCRVPMEDGDKRCKLLIGILVLLIIVILGVLPIITIKANSEACRDLAV 60

Qy 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120
Db 61 MECAVTHLLOQELTEAOKGFQDVEAOATCNHTVMALMASIDAKAOKQKVEELGEI 120

Qy 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172
Db 121 TTLNHLKODASAEVERLERENOVLSVRIADKKYYPSSQDSSAAAPOLLIVL 172

```

```

RESULT 13
US-10-428-085-5
Sequence 5, Application US/10428085
Publication No. US20030175281A1
GENERAL INFORMATION:
APPLICANT: KOSAKA, MASAOKI
APPLICANT: KOISHIHARA, YASUO
TITLE OF INVENTION: ENHANCER FOR ANTIBODY TO LYMPHOCTIC TUMORS
FILE REFERENCE: 053466/0276
CURRENT APPLICATION NUMBER: US/10/428,085
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US/09/509,530B
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: PCT/JP98/04645
PRIOR FILING DATE: 1998-10-14
PRIOR APPLICATION NUMBER: JP 10-222024
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: JP 9-280759
PRIOR FILING DATE: 1997-10-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-428-085-5

```

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 |||||  
 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 |||||  
 DB 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 |||||  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

## RESULT 14

US-10-423-007-3  
 ; Sequence 3, Application US/10423007  
 ; Publication No. US20030180889A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: OHTOMO, TOSHIHIKO  
 ; APPLICANT: TSUCHIYA, MASAYUKI  
 ; APPLICANT: KOISHIHARA, YASUO  
 ; APPLICANT: KOSAKA, MASAAKI  
 ; TITLE OF INVENTION: GENOMIC GENE ENCODING HM 1.24 ANTIGEN PROTEIN AND  
 ; FILE REFERENCE: 053466/0285  
 ; CURRENT FILING DATE: 2003-04-25  
 ; PRIOR FILING DATE: 2003-04-25  
 ; PRIOR APPLICATION NUMBER: US/09/622,166A  
 ; PRIOR FILING DATE: 2000-08-14  
 ; PRIOR APPLICATION NUMBER: PCT/JP99/00884  
 ; PRIOR FILING DATE: 1999-02-25  
 ; PRIOR APPLICATION NUMBER: 10-60617  
 ; PRIOR FILING DATE: 1998-02-25  
 ; PRIOR APPLICATION NUMBER: 10-93883  
 ; PRIOR FILING DATE: 1998-03-24  
 ; NUMBER OF SEQ ID NOS: 33  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 3  
 ; LENGTH: 180  
 ; TYPE: PRT  
 ; ORGANISM: Mus sp.  
 US-10-423-007-3

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 |||||  
 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 |||||  
 DB 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 |||||  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

## RESULT 15

US-10-257-021-80  
 ; Sequence 80, Application US/10257021  
 ; Publication No. US20030211498A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Morin, Patrice J.  
 ; APPLICANT: Sherman-Baust, Cheryl A.  
 ; APPLICANT: Pfizer, Ellen S.

APPLICANT: Hough, Colleen D.  
 ; TITLE OF INVENTION: TUMOR MARKERS IN OVARIAN CANCER  
 ; FILE REFERENCE: 14014.0369U2  
 ; CURRENT APPLICATION NUMBER: US/10/257,021  
 ; CURRENT FILING DATE: 2002-10-03  
 ; PRIOR APPLICATION NUMBER: PCT/US01/10947  
 ; PRIOR FILING DATE: 2001-04-03  
 ; PRIOR APPLICATION NUMBER: 60/194,336  
 ; PRIOR FILING DATE: 2000-04-03  
 ; NUMBER OF SEQ ID NOS: 147  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 80  
 ; LENGTH: 180  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-257-021-80

Query Match 100.0%; Score 854; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2e-74;  
 Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
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 DB 1 MASTSYDYCRVPMEDGDKCKLLIGIIVLLIIVILGVPLIIFTIKANSEACRDGLRAY 60  
 QY 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 |||||  
 DB 61 MECRNVTLLQOELTEAQKGFQDVEAQAATCNHTWALMASLDAEKAQOKKVEELGEI 120  
 QY 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172  
 |||||  
 DB 121 TTINHKLODASAEVERLRRENOVLSVRIADKKYPPSSODSSAAAPOLLIVL 172

Search completed: December 29, 2004, 11:41:12  
 Job time : 589 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:11:07 ; Search time 25 Seconds  
(without alignments)  
661.971 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854

Sequence: 1 MASTSYDYCRVPMEDGDKRC.....YTPSSQDSSAAAPQLLIVL 172

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_79:\*  
2: pir1:\*  
3: pir2:\*  
4: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Query Length | DB ID | Description                |
|------------|-------|-------------|--------------|-------|----------------------------|
| 1          | 854   | 100.0       | 180          | 2     | A56836 bone marrow stroma  |
| 2          | 111   | 13.0        | 778          | 2     | T30430 hypothetical prote  |
| 3          | 107.5 | 12.6        | 461          | 2     | H84099 cell wall-binding   |
| 4          | 107   | 12.5        | 423          | 2     | G83955 flagellar protein   |
| 5          | 104   | 12.2        | 423          | 2     | I59463 keratin, type I, c  |
| 6          | 102.5 | 12.0        | 1534         | 2     | A56734 ribosome receptor,  |
| 7          | 101.5 | 11.9        | 550          | 2     | A28166 Kupffer cell recept |
| 8          | 99.5  | 11.7        | 304          | 2     | JY0209 lectin, galactose/  |
| 9          | 99    | 11.6        | 415          | 2     | S35760 fcrA protein precu  |
| 10         | 98.5  | 11.5        | 1963         | 1     | MMKW myosin heavy chain    |
| 11         | 98    | 11.5        | 1938         | 1     | AMWKM myosin heavy chain   |
| 12         | 98    | 11.5        | 1938         | 1     | A59293 myosin heavy chain  |
| 13         | 97    | 11.4        | 286          | 2     | S07533 puf II/9A-2 prote   |
| 14         | 96.5  | 11.3        | 597          | 2     | S40998 hypothetical prote  |
| 15         | 96.5  | 11.3        | 893          | 2     | G88551 protein M01A8.2 (i  |
| 16         | 96    | 11.2        | 286          | 2     | S07532 puf II/9-1 protei   |
| 17         | 95    | 11.1        | 1937         | 2     | I38055 myosin heavy chain  |
| 18         | 95    | 11.1        | 1972         | 1     | A41604 myosin heavy chain  |
| 19         | 94.5  | 11.1        | 1972         | 1     | S76705 hypothetical prote  |
| 20         | 94    | 11.0        | 676          | 2     | S00084 myosin heavy chain  |
| 21         | 93.5  | 10.9        | 359          | 2     | H64629 hypothetical prote  |
| 22         | 93    | 10.9        | 359          | 2     | I50712 TOP AP - chicken    |
| 23         | 93    | 10.9        | 848          | 2     | A44972 paramyosin - nemat  |
| 24         | 93    | 10.9        | 879          | 2     | A48575 paramyosin - nemat  |
| 25         | 93    | 10.9        | 1938         | 2     | JC5421 smooth muscle myos  |
| 26         | 93    | 10.9        | 1938         | 2     | JC5420 smooth muscle myos  |
| 27         | 92.5  | 10.8        | 1972         | 2     | G95258 secreted 45 kd pro  |
| 28         | 92.5  | 10.8        | 392          | 2     | B98124 general stress pro  |
| 29         | 92.5  | 10.8        | 1388         | 2     | S74245 serine/threonine-s  |

|    |      |      |      |   |                           |
|----|------|------|------|---|---------------------------|
| 30 | 92.5 | 10.8 | 1938 | 1 | S06005 myosin alpha heavy |
| 31 | 92.5 | 10.8 | 1939 | 2 | I48175 myosin heavy chain |
| 32 | 92   | 10.8 | 866  | 2 | S04027 paramyosin - Caeno |
| 33 | 92   | 10.8 | 872  | 2 | T19296 hypothetical prote |
| 34 | 91.5 | 10.7 | 746  | 2 | T47237 myosin II heavy ch |
| 35 | 91.5 | 10.7 | 1938 | 2 | I49464 alpha cardiac myos |
| 36 | 91.5 | 10.7 | 2442 | 2 | T08621 centrosome associa |
| 37 | 91   | 10.7 | 507  | 2 | S05542 hypothetical prote |
| 38 | 91   | 10.7 | 741  | 2 | S39082 myosin heavy chain |
| 39 | 91   | 10.7 | 955  | 2 | S24348 myosin heavy chain |
| 40 | 90.5 | 10.6 | 244  | 2 | I36913 beta-myosin heavy  |
| 41 | 90.5 | 10.6 | 764  | 2 | I51302 myosin heavy chain |
| 42 | 90.5 | 10.6 | 1039 | 2 | S18199 myosin heavy chain |
| 43 | 90.5 | 10.6 | 1509 | 1 | A27224 myosin heavy chain |
| 44 | 90.5 | 10.6 | 1846 | 2 | A59289 myr 6, uncorventio |
| 45 | 90.5 | 10.6 | 1934 | 2 | I48153 myosin heavy chain |

## ALIGNMENTS

```

RESULT 1
A56836
bone marrow stromal cell surface protein BST-2 - human
C:Species: Homo sapiens (man)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56836
R:Rishikawa, J.; Kaisho, T.; Tomizawa, H.; Lee, B.O.; Kobune, Y.; Inazawa, J.; Oritani, K
Genomics 26, 527-534, 1995
A>Title: Molecular cloning and chromosomal mapping of a bone marrow stromal cell surface
A:Reference number: A56836; MUID:95331788; PMID:7607676
A:Accession: A56836
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-180 <ISH>
A:Cross-references: UNIPROT:Q10589; GB:D28137; NID:9457563; PIDN:BAA05679.1; PID:G506861
C:Genetics:
A:Gene: GDB:BST2
A:Cross-references: GDB:409946; OMIM:600534
A:Map position: 19p13.2-19p13.2
C:Keywords: transmembrane protein

Query Match          100.0%; Score 854; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 2,2e-60;
Matches 172; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MASTSYDYCRVPMEDGDKRCALLGIGLVLLIIVIGVPIIFTIKANSEACRDGLRAV 60
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DB       1 MASTSYDYCRVPMEDGDKRCALLGIGLVLLIIVIGVPIIFTIKANSEACRDGLRAV 60
        |||

QY      61 MECNRYVTHLLOOELTEAKGQDVEAOATGNTVMMAISLDEKAGQKVELEGEI 120
        |||
DB       61 MECNRYVTHLLOOELTEAKGQDVEAOATGNTVMMAISLDEKAGQKVELEGEI 120
        |||

QY      121 TTNHKLQDASAEYERLRERNOVLVRIADKKYTPSSQDSSAAAPQLLIVL 172
        |||
DB       121 TTNHKLQDASAEYERLRERNOVLVRIADKKYTPSSQDSSAAAPQLLIVL 172
        |||

RESULT 2
T30430
hypothetical protein ORF82 - Lymantria dispar nuclear polyhedrosis virus
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdNPV
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C:Accession: T30430
R:Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr
Virology 253, 17-34, 1999
A>Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d
A:Reference number: Z20836; MUID:99124785; PMID:9887315
A:Accession: T30430
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-778 <KUZ>

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A:Cross-references: UNIPROT:Q9YMP5; EMBL:AF081810; PIDD:AACT0268.1

Query Match 13.0%; Score 111; DB 2; Length 778;  
Best Local Similarity 32.5%; Pred. No. 0.38;  
Matches 38; Conservative 22; Mismatches 47; Indels 10; Gaps 4;

QY 46 IKANSEACRDGLRAWECEK-NVTHLLQOELTEAQKGFQVEAQAATCNHTVMAIASIDA 104  
DB 520 LKAQSELRND-LQAKRAQADANARLQAEIDSLK-ASDADLRNRVAVQLAEAAES 574

QY 105 EKAQOQKVEELLEGITTLNHLQDASAEVERLRRENOVLVRIADKTYPSQDS 161  
DB 575 GAADQNRIRARLEAESSGLTRLOSAAEVLAALRRDKEDLERRTAAS-AAQDVS 627

RESULT 3  
cell wall-binding protein BH3600 [imported] - Bacillus halodurans (strain C-125)  
H84099  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: H84099  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: H84099  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-461 <STO>  
A:Cross-references: UNIPROT:Q9K6X4; GB:AP001519; GB:BA000004; NID:G10176109; PIDD:BA0073  
A:Experimental source: strain C-125  
C:Genetics:

A:Gene: BH3600

Query Match 12.6%; Score 107.5; DB 2; Length 461;  
Best Local Similarity 26.1%; Pred. No. 0.42;  
Matches 31; Conservative 28; Mismatches 55; Indels 5; Gaps 2;

QY 33 IIVILGVPIITFIKANSEACRDGLRAWECEKRVTHLLQOELTEAQKGFQVEAQAATCN 92  
DB 5 ISLVAAAGLITRISLFSQSIEDA-KANSSLOQISDVOKERQKQOKTEAL- 59

QY 93 HTVMALMASIDAEKAQOKKVELEGEITTLNHLQDASAEVERLRRENOVLVRIADK 151  
DB 60 KEVEKELGDTAEIRLDEKVERTSGKIQEKREIREVOAETELKEQJLEIRIAR 118

RESULT 4  
flagellar protein required for flagellar formation flil [imported] - Bacillus halodurans  
G83955  
C:Species: Bacillus halodurans  
C>Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
C:Accession: G83955  
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maui, N.; Fuji, F.; Hirai  
Nucleic Acids Res. 28, 4317-4331, 2000  
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
A:Reference number: A83650; MUID:20512582; PMID:11058132  
A:Accession: G83955  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-143 <STO>  
A:Cross-references: UNIPROT:Q9KA43; GB:AP001515; GB:BA000004; NID:G10174886; PIDD:BA0061  
A:Experimental source: strain C-125  
C:Genetics:

A:Gene: flil

Query Match 12.5%; Score 107; DB 2; Length 143;  
Best Local Similarity 22.1%; Pred. No. 0.14;  
Matches 31; Conservative 34; Mismatches 49; Indels 26; Gaps 4;

QY 23 LIGIGLVLLIIVLGVPIITFIKANSEACRDGLRAWECEK-NVTHLLQOEL 74  
DB 6 LVNIMILIIIVLTVGVAVLIFVNYFNNEDEQDREPTIDELIAQSYETEITTLISNDF 65

QY 75 TEA-----QKGFQVEAQAATCNHTVMAIASIDAEKAQOQKVELEGEITTLNHLK 126  
DB 66 VRARLTHVDNRNMLQFQKRDFOVNNIIIRSLAGMDASQSGADGIEKLAQ----- 118

QY 127 LODASAEVERLRRENOVLV 146  
DB 119 LQD--DINALMQEGSVVKI 135

RESULT 5  
159463  
keratin, type I, cytoskeletal - mouse  
N.Alternate names: endo B cytokeratin; keratin D  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
C:Accession: I59463; A25621; K28428; J00406  
R:Alonso, A.; Weber, T.; Jorcano, J.L.  
Roux's Arch. Dev. Biol. 196, 16-21, 1987  
A>Title: Cloning and characterization of keratin D, a murine endodermal cytoskeletal pro  
A:Reference number: I59463  
A:Accession: I59463  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-423 <RES>  
A:Cross-references: UNIPROT:P05784; GB:M36376; NID:G198587; PIDD:AAA9373.1; PID:G293682  
R:Singer, P.A.; Trevor, K.; Oshima, R.G.  
J. Biol. Chem. 261, 538-547, 1986  
A>Title: Molecular cloning and characterization of the endo B cytokeratin expressed in p  
A:Reference number: A25621; MUID:8608576; PMID:2416755  
A:Accession: A25621  
A:Molecule type: mRNA  
A:Residues: 1-243, 'D', 245-252, 'A', 254-423 <SIN>  
A:Cross-references: GB:M11686; NID:G198620; PIDD:AAA39390.1; PID:G293685  
R:Oshima, R.G.; Trevor, K.; Shevinsky, L.H.; Ryder, O.A.; Cecena, G.  
Genes Dev. 2, 505-516, 1988  
A>Title: Identification of the gene coding for the endo B murine cytokeratin and its met  
A:Reference number: A28428; MUID:88255838; PMID:2454868  
A:Accession: A28428  
A:Molecule type: DNA  
A:Residues: 1-132 <OSH>  
A:Cross-references: GB:Y00217; NID:G50842; PIDD:CAA68365.1; PID:G50843  
R:Ichinose, Y.; Morita, T.; Zhang, F.; Strimashov; S.; Tondella, M.L.C.; Matsumoto,  
Gene 70, 85-95, 1988  
A>Title: Nucleotide sequence and structure of the mouse cytokeratin endoB gene.  
A:Reference number: J00406; MUID:89196920; PMID:2467843  
A:Accession: J00406  
A:Molecule type: DNA  
A:Residues: 1-133, 'F', 135-243, 'D', 245-252, 'A', 254-423 <ICH>  
A:Cross-references: GB:M2832; NID:G340757; PIDD:AAA37552.1; PID:G532610  
C:Genetics:  
A:Gene: endoB; KERD  
A:Introns: 132/3; 160/2; 212/3; 267/3; 309/3; 384/2  
C:Superfamily: cytoskeletal keratin  
C:Keywords: coiled coil; intermediate filament

Query Match 12.2%; Score 104; DB 2; Length 423;  
Best Local Similarity 28.5%; Pred. No. 0.73;  
Matches 43; Conservative 24; Mismatches 42; Indels 42; Gaps 7;

QY 44 FTIKANSE-ACD-----GIRAMECRNVTHL-----LQOELTEAQKGFQD 83  
DB 157 FVFKVETELAMQSVESDIHGKRVDDTNITRLLETEIALKEELLFMKONHEBEVOG 216

QY 84 VEAQAATCNHTV-----MALMASIDAE-KAQOQKVELE-----GEIT 121  
DB 217 LBAQIASSGLIVEVAPKSDISKIMANIRAOYEALGQKREELDKYMSQGLESTTVT 276

QY 122 TLNHLQDASAEVERLRRENOVLVRIADK 152  
DB 277 TKSARIRDAETTLTELRLQLLEIDLSMK 307



RESULT 6  
A56734  
ribosome receptor, 180K - dog  
C:Species: Canis lupus familiaris (dog)  
C>Date: 08-Jul-1995 #sequence\_revision 03-Aug-1995 #text\_change 09-Jul-2004  
C:Accession: A56734  
R:Walker, E.E.; Sun, Y.; Savitz, A.J.; Meyer, D.I.  
J. Cell Biol. 130, 29-39, 1995  
A:Title: Functional characterization of the 180-KD ribosome receptor in vivo.  
A:Reference number: A56734; MUID:95310363; PMID:7790375  
A:Accession: A56734  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-1534 <MAN>  
A:Cross-references: UNIPROT:Q28298; GB:X87224; NID:984113; PIDN:CAA6076.1; PID:984114  
C:Keywords: endoplasmic reticulum; membrane protein; protein biosynthesis  
F:198-743/Region: 10-residue repeats (N-Q-G-K-K-A-E-G-A-P)

Query Match 12.0%; Score 102.5; DB 2; Length 1534;  
Best Local Similarity 28.6%; Pred. No. 3.6;  
Matches 26; Conservative 22; Mismatches 42; Indels 1; Gaps 1;

Qy 55 DGLRAWEKCRNVTHLLQDELTEAOKGFQDVEAQAATCNHTWALMASLDAEKAQCKYK 114  
Db 847 DAAVAKSKLRVKNKEIAAEKAAAGAKVKQIVARSOEITVAQARIEASYREHVEQV 906  
Qy 115 ELEGEITLNNKLODA-SAEVERLRRENOVL 144  
Db 907 QLOGKIRTLQEDLENGPNTQLAKLQDENSIL 937

RESULT 7  
A28166  
Kupffer cell receptor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 09-Jul-2004  
C:Accession: A28166  
R:Hoyle, G.W.; Hill, R.L.  
J. Biol. Chem. 266, 1850-1857, 1991  
A:Title: Structure of the gene for a carbohydrate-binding receptor unique to rat Kupffer  
A:Reference number: A28166; MUID:91107689; PMID:1846367  
A:Accession: A28166  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-550 <HO2>  
A:Cross-references: UNIPROT:P10716; GB:M55532; NID:9203362; PIDN:AAA40892.1; PID:9203363  
R:Hoyle, G.W.; Hill, R.L.  
J. Biol. Chem. 263, 7487-7492, 1988  
A:Title: Molecular cloning and sequencing of a cDNA for a carbohydrate binding receptor  
A:Reference number: A28166; MUID:88227939; PMID:2836387  
A:Accession: A28166  
A:Molecule type: mRNA  
A:Residues: 1-550 <HOY>  
A:Cross-references: GB:J03734; NID:9205050; PIDN:AAA41472.1; PID:9205051  
C:Keywords: transmembrane protein  
F:412-536/Domain: C-type lectin homology <LCH>

Query Match 11.9%; Score 101.5; DB 2; Length 550;  
Best Local Similarity 26.0%; Pred. No. 1.5;  
Matches 32; Conservative 22; Mismatches 58; Indels 11; Gaps 2;

Qy 46 IKANEACRQDGLRAWEKCRNVTHLLQDELTEAOKGFQDVEAQAATCNHTWALMASLDAE 105  
Db 256 ISAEIQARQDGMQRGE-----EMTSIAKULETITTAQIQANGLBETDTQIQGL 305  
Qy 106 KAQCGKVELEGEITLNNKLODA-SAEVERLRRENOVL-SVRIADKKYPPSQDSSAA 165  
Db 306 KAQ-IGKSTSSINSQIEVNVGKLDSSRELQTLRRDLSDVSAKSNVQMLQAKAKAV 364  
Qy 166 PQL 168  
Db 365 QSL 367

RESULT 8  
UX0209  
lectin, galactose/N-acetylglactosamine-specific - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: UX0209; PX0009  
R:Sato, M.; Kawakami, K.; Osawa, T.; Toyoshima, S.  
J. Biochem. 111, 331-336, 1992  
A:Title: Molecular cloning and expression of cDNA encoding a galactose/N-acetylglactosa  
A:Reference number: UX0209; MUID:92268032; PMID:1587794  
A:Accession: UX0209  
A:Molecule type: mRNA  
A:Residues: 1-304 <SAT>  
A:Cross-references: UNIPROT:P49300; GB:S36676; NID:9249360; PIDN:AAB22171.1; PID:9249361  
R:Oda, S.; Sato, M.; Toyoshima, S.; Osawa, T.  
J. Biochem. 104, 600-605, 1988  
A:Title: Purification and characterization of a lectin-like molecule specific for galact  
A:Reference number: PX0009; MUID:89197865; PMID:3241002  
A:Accession: PX0009  
A:Molecule type: protein  
A:Residues: 102-120:137, 'X', 139-151 <ODA>

C:Superfamily: hepatic lectin; C-type lectin homology  
C:Keywords: glycoprotein; lectin; macrophage; transmembrane protein  
F:36-61/Domain: transmembrane #status predicted <TRA>  
F:173-296/Domain: C-type lectin homology <LCH>  
F:74.166/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 11.7%; Score 99.5; DB 2; Length 304;  
Best Local Similarity 23.2%; Pred. No. 1.2;  
Matches 36; Conservative 37; Mismatches 49; Indels 33; Gaps 7;

Qy 24 LGIGLVLLIVLIGVPLIFITKANSEACRD--GLRAWEKCRNVTHLLQDELTEAOKGF 81  
Db 41 LGLSHLLVAVSVIG-----SONSQLRDLGLTRATLD--NTSKIKAE-----F 83  
Qy 82 QDVEAQAATCNHTWALMASLDAEKAQCKYK-----KVEELEGEI-----TTNNKLODAS 131  
Db 84 QSLDRADSFKEGSISSLKVDVEDHRLQAGRDLQKVTSLSTVEKKEQALKTDLSDLT 143  
Qy 132 SAVERLRRENOVL-SVRIADKKYPPSQDSSAAAP 166  
Db 144 DHVQQLRKDLKALTCQLANLK---NNGSEVACCP 174

RESULT 9  
S35760  
ferritin precursor - Streptococcus pyogenes  
C:Species: Streptococcus pyogenes  
C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S35760; A42711  
R:Podbielski, A.  
submitted to the EMBL Data Library, November 1992  
A:Reference number: S35760  
A:Accession: S35760  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-415 <POD>  
A:Cross-references: UNIPROT:O54859; EMBL:X69324; NID:9311759; PIDN:CAA49165.1; PID:93117  
J:Haanes, E.J.; Heath, D.G.; Cleary, P.P.  
J. Bacteriol. 174, 4967-4976, 1992  
A:Title: Architecture of the vir regulons of group A streptococci parallels opacity fact  
A:Reference number: A42711; MUID:92332431; PMID:1385809  
A:Accession: A42711  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 343-415 <HAA>  
A:Cross-references: NID:M66806; NID:9153630; PIDN:AAA26887.1; PID:9153631  
A:Experimental source: strain CS101, OF+  
A:Note: sequence extracted from NCBI backbone (NCBI:108942, NCBI:108945)  
C:Superfamily: M5 protein

Query Match 11.6%; Score 99; DB 2; Length 415;

[illegible]

```

F:1163-1963/Region: light meromyosin
F:1163/Modified site: N6,N6,N6-trimethyllysine (Lys) #status predicted
F:180/Binding site: ATP (Lys) #status predicted
F:702,712/Active site: Cys #status predicted

Query Match          11.5%; Score 98.5; DB 1; Length 1963;
Best Local Similarity 24.7%; Pred. No.: 9, 6;
Matches 36; Conservative 21; Mismatches 58; Indels 31; Gaps 5;

OY 47 KANSACDGLRAVNECRVTHLLQQLLEAQQKGFQDVEQAATCNHTWALWASLAAEK 106
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1808 EAFAALGKGGKVIATLEQVRELSELDGEQRFQDANKNLGRADRVRELQFQVEDBK 1867
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 107 AQ-----GKKVLELEGETTLN-----HKLDASAEVRLRREN 141
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1668 KNFRLQDLIDLEQKTKQKQVEAE-ELANLNLQKKYKQLHQLDAERAD--QAEN 1924
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 142 QVLSVRI--ADKKYPPSSQSSSSAA 164
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1925 SLSKRSKSRASASVAFGLQSSASAA 1950
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
MKKW1
myosin heavy chain D [similarity] - Caenorhabditis elegans
N:Alternate names: myosin heavy chain I
N:Contains: myosin ATPase (EC 3.6.4.1)
C:Species: Caenorhabditis elegans
C:Date: 28-Feb-1986 #sequence revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: T21193; T23973; S02772; A02993
R:McMurray, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19388
A:Accession: T21193
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1938 <W1>
A:Cross-references: UNIPROT:P02567; EMBL:Z71261; PDB:CAA95806.1; GSPDB:GN00019; CESP:R0
A:Experimental source: clone F21C3
R:Gardner, A.
submitted to the EMBL Data Library, April 1996
A:Reference number: Z19825
A:Accession: T23973
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1938 <W12>
A:Cross-references: EMBL:Z71266; PDB:CAA95848.1; GSPDB:GN00019; CESP:R06C7.10
A:Experimental source: clone R06C7
R:Diib, N.J.; Maruyama, I.N.; Krause, M.; Karn, J.
J. Mol. Biol. 205, 603-613, 1989
A:Title: Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gen
A:Reference number: S02771; M01D:89178677; PMID:2926820
A:Accession: S02772
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-376 'V', 378-390, 'V', 392-576, 'L', 578-680, 'I', 682-1938 <DIB>
A:Cross-references: EMBL:X08065; NID:g6785; PDB:CAA30854.1; PID:g6786
R:Karn, U.; Bremer, S.; Barnett, L.
Proc. Natl. Acad. Sci. U.S.A. 80, 4253-4257, 1983
A:Title: Protein structural domains in the Caenorhabditis elegans unc-54 myosin heavy ch
A:Reference number: A93958; M01D:83273600; PMID:6576334
A:Accession: A02993
A:Molecule type: DNA
A:Residues: 24-93, 'E', 95-97, 'R', 99-376, 'V', 378-388, 'GDV', 392-407, 'N', 409-473, 'G', 475-576
C:Genetics:
A:Gene: myo-1; CESP:R06C7.10
A:Map position: 1
A:Introns: 23/3; 114/3; 229/1; 264/1; 320/1; 857/3; 1745/3; 1814/1; 1892/3
C:Superfamily: myosin heavy chain; myosin motor domain homology
C:Keywords: actin binding; ATP; coiled coil; hydrolase; methylated amino acid; muscle cc
F:177-184/Region: nucleotide-binding motif A (p-loop)
F:660-682/Region: actin binding #status predicted

```

F:764-778/Region: actin binding #status predicted  
 F:846-1938/Domain: coiled coil #status predicted <COI>  
 F:846-1160/Region: S2  
 F:1161-1938/Region: light meromyosin  
 F:126/Modified site: N6/N6, N6-trimethyllysine (lys) #status predicted  
 F:189/Binding site: ATP (lys) #status predicted  
 F:700,710/Active site: Cys #status predicted

Query Match 11.5%; Score 98; DB 1; Length 1938;  
 Best Local Similarity 26.6%; Pred. No. 10;  
 Matches 34; Conservative 24; Mismatches 58; Indels 12; Gaps 4;

QY 51 EACRDGLRAVME---CERNVTHLQQ--ELTEAQ-KGFQDVEAQAATCNHTVMALMSID 103  
 DB 1324 KAABDELHERQEFNAACNLEHLDQCHLEEQINGKDIQRLSRINSEISQWKARYE 1383  
 QY 104 AEKAGQGVKEVELEGEITTLNHLQDASAEVERLRERNOVSRLADKKYVSSQDSSSA 163  
 DB 1384 GEGLVSESELEELKKQNNRMVMDLQELASAA-----QNKVLSLEKAKGLLAETEDARSD 1438  
 QY 164 AAPQLLIV 171  
 DB 1439 VDRHLTVI 1446

RESULT 12  
 A59293  
 skeletal myosin heavy chain - domestic rabbit  
 C:Species: Oryctolagus cuniculus  
 C>Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004  
 C:Accession: A59293  
 R:Maeda, K.; Hostinova, E.; Roesc, Kleinkauf, A.; Schuster, H.; Gaeperik, J.; Wittinghofer  
 submitted to GenBank, July 1995  
 A:Description: Isolation, sequencing of myosin heavy chain cDNA from rabbit skeletal mus  
 A:Reference number: A59293  
 A:Accession: A59293  
 A:Status: preliminary; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-1938 <MAE>  
 A:Cross-references: UNIPROT:028641; GB:U32574; NID:G940232; PIDN:AAA74199.1; PID:G94023  
 A:Experimental source: strain New Zealand White; cell type skeletal muscle fiber type II  
 C:Genetics:  
 A:Gene: MYH  
 C:Superfamily: myosin heavy chain; myosin motor domain homology  
 F:89-769/Domain: myosin motor domain homology <MMO>

Query Match 11.5%; Score 98; DB 2; Length 1938;  
 Best Local Similarity 26.1%; Pred. No. 10;  
 Matches 37; Conservative 20; Mismatches 45; Indels 40; Gaps 5;

QY 47 KANSEACR-----DGLRAVMECRNVTHLQOELTEAQKGFQDVEAQAATCNHTVMALM 99  
 DB 1366 KANSEVAAQWRKYETDIAQRTLEAEAKKLAQRLQDAE--EHYEAVNAKC----- 1414  
 QY 100 ASLDAEKAQGVKEVELEGEITTLN-----HKLQDASAEVERLR 138  
 DB 1415 ASLEKTKQRLQVEVDLMIDVERTNAACALDKQRPNDKILAEWKHYETHALELSQ 1474  
 QY 139 RENQVLSVRIAD-KKYVPSQD 159  
 DB 1475 KESRSLSTEVEFKVNAYESID 1496

RESULT 13  
 S07533  
 puf II/9A-2 protein precursor - fungus gnat (Sciara coprophila)  
 C:Species: Sciara coprophila  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C:Accession: S07533  
 R:DiBartolomeis, S.M.; Gerbi, S.A.  
 J.Mol. Biol. 210, 531-540, 1989  
 A>Title: Molecular characterization of DNA puf II/9A genes in Sciara coprophila.  
 A:Reference number: S07532; MUID:90133907; PMID:2614832

A:Accession: S07533  
 A:Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-286 <DIB>  
 A:Cross-references: UNIPROT:P22312; GB:X51679; NID:g10113; PID:g1405812  
 C:Genetics:  
 A:Map position: II/9A  
 C:Keywords: coiled coil; glycoprotein  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-286/Product: puf II/9A protein #status predicted <MAT>  
 F:156/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 11.4%; Score 97; DB 2; Length 286;  
 Best Local Similarity 25.6%; Pred. No. 1.8;  
 Matches 31; Conservative 24; Mismatches 36; Indels 30; Gaps 5;

QY 46 IKANSEACRDGLRAVMECRNVTHLQOELTEAQKGFQDVEAQAATCNHTVMAL 98  
 DB 89 LKREKARQKAEKAEQKNTENKETTEQLKSLARQALKCKELADCK----- 142  
 QY 99 MASLDAEKAQGVKEVELEGEITTLNHLQ-----DASAEVERLRRE---NQVLSV 146  
 DB 143 -----KENAKLNTKIEBLNCTTTOQLERGRGRERLQQLDCKKKKNTCNNEILLAC 197  
 QY 147 R 147  
 DB 198 R 198

RESULT 14  
 S40998  
 hypothetical protein M01A8.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C:Accession: S40998  
 R:Hawkins, I.; Thomas, K.  
 submitted to the EMBL Data Library, October 1993  
 A:Reference number: S40997  
 A:Accession: S40998  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-597 <HAN>  
 A:Cross-references: EMBL:Z27081  
 C:Genetics:  
 A:Introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1

Query Match 11.3%; Score 96.5; DB 2; Length 597;  
 Best Local Similarity 24.8%; Pred. No. 4.1;  
 Matches 32; Conservative 29; Mismatches 39; Indels 29; Gaps 4;

QY 48 ANSEACRDGLRAVMECRNVTHLQOELTEAQKGFQDV---EQAATCNHTVMALMS 101  
 DB 270 SNOQVIRHANAV-ESLQKTHETQIAEKKEPERNFEEERARRAEVCAANNRHQKVAC 328  
 QY 102 LDAEKAQGVKEVELE-----GEITTLNHLQDASAEVERLR 139  
 DB 329 IDEKISBAEQCEQLNVQKVLQALANDCDHRNQMLTKETISLQFALMSKAEKELRQ 388  
 QY 140 ENQVLSVRI 148  
 DB 389 KNQNLSTQV 397

RESULT 15  
 G88551  
 protein M01A8.2 [imported] - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 C:Accession: G88551  
 R:anonymous, The C. elegans Sequencing Consortium.  
 Science 282, 2012-2018, 1998  
 A>Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
 A:Reference number: A75000; MUID:99069613; PMID:9851916



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 29, 2004, 11:31:07 ; Search time 104 Seconds

(without alignments)  
951.581 Million cell updates/sec

Title: US-10-069-290A-2

Perfect score: 854

Sequence: 1 MASTSYDQCRVPMEDGDRRC.....YPPSSQDSSAAAPQLITVL 172

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID            | Description        |
|------------|-------|-------------|--------|---------------|--------------------|
| 1          | 854   | 100.0       | 180    | 1 BSTR2 HUMAN | Q10589 homo sapien |
| 2          | 297.5 | 34.8        | 203    | 2 O6WRU0      | Q6WRU0 cricetulus  |
| 3          | 297.5 | 34.8        | 203    | 2 AAO16301    | AAO16301 cricetulu |
| 4          | 271   | 31.7        | 172    | 2 O8R2Q8      | O8R2Q8 mus musculu |
| 5          | 229.5 | 26.9        | 172    | 2 O811A2      | O811A2 rattus norv |
| 6          | 162.5 | 19.0        | 108    | 2 O8CEY7      | O8CEY7 mus musculu |
| 7          | 111   | 13.0        | 778    | 2 O9YMP5      | O9YMP5 lymantria d |
| 8          | 107.5 | 12.6        | 461    | 2 O9K6X4      | O9K6X4 bacillus ha |
| 9          | 107   | 12.5        | 433    | 2 O9K6X4      | O9K6X4 bacillus ha |
| 10         | 104.5 | 12.2        | 560    | 2 O7ZTT2      | O7ZTT2 brachydanto |
| 11         | 104.5 | 12.2        | 782    | 1 HCR_PANPA   | O8H57 pan paniscu  |
| 12         | 104.5 | 12.2        | 782    | 1 HCR_PANTR   | O8H57 pan paniscu  |
| 13         | 104   | 12.2        | 900    | 2 O7R6H3      | O7R6H3 giardia lam |
| 14         | 103   | 12.1        | 782    | 1 HCR_PONPY   | O8H58 pongo pygma  |
| 15         | 102.5 | 12.0        | 621    | 2 O7Q003      | O7Q003 giardia lam |
| 16         | 102.5 | 12.0        | 1534   | 2 R8R1 CANPA  | O28298 canis famli |
| 17         | 102.5 | 12.0        | 1627   | 2 O7R264      | O7R264 giardia lam |
| 18         | 102.5 | 12.0        | 1627   | 2 O962Q0      | O962Q0 giardia lam |
| 19         | 101.5 | 11.9        | 304    | 2 O91Y73      | O91Y73 mus musculu |
| 20         | 101.5 | 11.9        | 507    | 2 O8CHM5      | O8CHM5 mus musculu |
| 21         | 101.5 | 11.9        | 526    | 2 O8CHM5      | O8CHM5 mus musculu |
| 22         | 101.5 | 11.9        | 550    | 1 KUCR_RAT    | P10716 rattus norv |
| 23         | 101.5 | 11.9        | 782    | 1 HCR_HUMAN   | O8C31 homo sapien  |
| 24         | 101.5 | 11.9        | 826    | 1 O9YHDS      | O9YHDS rana catesb |
| 25         | 101   | 11.8        | 782    | 1 HCR_GORGO   | O8H59 gorilla gor  |
| 26         | 101   | 11.8        | 782    | 1 O765H0      | O765H0 homo sapien |
| 27         | 101   | 11.8        | 782    | 2 BAD05130    | BAD05130 homo sapi |
| 28         | 101   | 11.8        | 782    | 2 BAD05131    | BAD05131 homo sapi |
| 29         | 100   | 11.7        | 865    | 2 O98SN6      | O98SN6 gallus gall |
| 30         | 99.5  | 11.7        | 270    | 2 P79391      | P79391 bos taurus  |
| 31         | 99.5  | 11.7        | 304    | 1 MMGL_MOUSE  | P49300 mus musculu |

|    |      |      |      |            |                     |
|----|------|------|------|------------|---------------------|
| 32 | 99.5 | 11.7 | 304  | 2 AAD31028 | AAO1028 mus muscu   |
| 33 | 99.5 | 11.7 | 708  | 2 O9YHD7   | O9YHD7 rana catesb  |
| 34 | 99.5 | 11.7 | 980  | 2 O73ML2   | O73ML2 treponema d  |
| 35 | 99.5 | 11.7 | 980  | 2 AAS12013 | AAS12013 treponema  |
| 36 | 99.5 | 11.7 | 1130 | 2 O86IC6   | O86IC6 dictyosteli  |
| 37 | 99.5 | 11.7 | 1622 | 2 O80224   | O80224 brachydanto  |
| 38 | 99.5 | 11.7 | 1932 | 2 O98TQ4   | O98TQ4 notothenia   |
| 39 | 99   | 11.6 | 415  | 2 O54859   | O54859 streptococc  |
| 40 | 99   | 11.6 | 800  | 2 O96X03   | O96X03 emericella   |
| 41 | 98.5 | 11.5 | 601  | 2 O6CUP5   | O6CUP5 gastrosoru   |
| 42 | 98.5 | 11.5 | 601  | 2 AAS19755 | AAS19755 gastrosoru |
| 43 | 98.5 | 11.5 | 782  | 2 O61AC8   | O61AC8 homo sapien  |
| 44 | 98.5 | 11.5 | 782  | 2 CAG33508 | CAG33508 homo sapi  |
| 45 | 98.5 | 11.5 | 975  | 2 O98TQ5   | O98TQ5 notothenia   |

## ALIGNMENTS

### RESULT 1

BSTR2\_HUMAN STANDARD; PRT; 180 AA.

AC Q10589;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Bone marrow stromal antigen 2 (BSTR-2).  
GN Name=BSTR2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
[1] SEQUENCE FROM N.A.  
RX MEDLINE=95331788; PubMed=7607676;  
RA Ishikawa J., Kaisho T., Tomizawa H., Lee B.O., Kobune Y., Inazawa J.,  
RA Ohtani K., Itoh M., Ochi T., Ishihara K., Hirano T.;  
RT "Molecular cloning and chromosomal mapping of a bone marrow stromal  
cell surface gene, BSTR2, that may be involved in pre-B-cell growth.";  
RL Genomics 26:527-534(1995).  
RN [2]  
[2] SEQUENCE FROM N.A.  
RP TISSUE=Blood;  
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stastewicz M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Mullahy S.J.,  
RA Paba S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyik S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U.A.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: May be involved in pre-B-cell growth.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.  
CC -!- TISSUE SPECIFICITY: Predominantly expressed in liver, lung, heart  
and placenta. Lower levels in pancreas, kidney, skeletal muscle  
and brain.  
CC -!- DISEASE: May play a role in B-cell activation in rheumatoid  
arthritis (RA).  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration



RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
RC Expression driven by an MMTV-LTR enhancer.;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
Dichtenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Ueda T.B., Toshiyuki S., Carrinci P., Prange C.,  
Raha S.S., Locuclano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CZECH II;  
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Wnt1 model.  
RC Expression driven by an MMTV-LTR enhancer.;  
RA Straubeberg R.;  
RL Submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC027328; AAH27328.1; -  
DR MGI; MGI:1916800; 2310015110Rik.  
SQ SEQUENCE 172 AA; 19152 MW; A2032FD01PAF601A CRC64;  
  
Query Match 31.7%; Score 271; DB 2; Length 172;  
Best Local Similarity 39.8%; Pred. No. 1.5e-13;  
Matches 72; Conservative 27; Mismatches 56; Indels 26; Gaps 6;  
  
QY 1 MASTSYDVCYPMED-----GDKRCKLLGIGILVLLIIVLIGVLIIFTIKANSEACRD 55  
DB 1 MAPSFYHLPVPMDEMRPKGMSIRRMVLVAAILVVLIGVLIIFTIKANSEACRD 60  
QY 56 GLRAVMECRNYTHLQOEITLTAQKGFODVEAQAATCNHTVAMLSDAEKAGCK---K 112  
DB 61 GLRAQAEGRNTTHLQRLQTLRTQDSLLQAEQAQNSCNLTIVTLQSLKKSQALEQOAR 120  
QY 113 VBELEGITTLNHLQDASAEVERLRRENQVLS-VRIDKTKYPSQDSSGAAPQLIV 171  
DB 121 IKELNEVTKLNQ-----ELENLRIQKETSSTVQV-----NSGSMVVSSILV 163  
QY 172 L 172  
DB 164 L 164  
  
RESULT 5  
Q811A2 PRELIMINARY; PRT; 172 AA.  
AC Q811A2;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE DAMP-1 protein.  
GN Name=damp-1;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wiistar; TISSUE=Liver;  
RA Kupzig S.;  
RT "Identification and characterisation of two novel proteins of the

RT secretory pathway.";  
RL Theiss (1998), Department of Biochemistry, University of Bristol,  
RL Bristol, United Kingdom.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wiistar; TISSUE=Liver;  
RA Kupzig S., Korolchuk V., Rolison R., Sugden A.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wiistar; TISSUE=Liver;  
RA Banting G.;  
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ538349; CAD61869.1; -  
SQ SEQUENCE 172 AA; 19674 MW; 5B1018EBBDD0FB19 CRC64;  
  
Query Match 26.9%; Score 229.5; DB 2; Length 172;  
Best Local Similarity 39.1%; Pred. No. 2.8e-10;  
Matches 59; Conservative 25; Mismatches 52; Indels 15; Gaps 3;  
  
QY 1 MASTSYDVCYPMED-----GDKRCKLLGIGILVLLIIVLIGVLIIFTIKANSEACRD 55  
DB 1 MAPSFYHLPVPMDEMRPKGMSIRRMVLVAAILVVLIGVLIIFTIKANSEACRD 60  
QY 56 GLRAVMECRNYTHLQOEITLTAQKGFODVEAQAATCNHTVAMLSDAEKAGCK---K 112  
DB 61 GLRLQDECRNTTHLKHQLTRAQDSLLQTEMQAQNSCNQTVMDLRSLKKSQTFEQOAR 120  
QY 113 VBELEGITTLNHLQDASAEVERLRRENQV 143  
DB 121 IKELNEKTLERLNQ-----ELENLRTQKEI 144  
  
RESULT 6  
Q8CEY7 PRELIMINARY; PRT; 108 AA.  
AC Q8CEY7;  
DT 01-MAR-2003 (TRENBLrel. 23, Created)  
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
DE Mus musculus adult male tongue cDNA, RIKEN full-length enriched  
DE library, clone:2310015110 product:hypothetical protein, full insert  
DE sequence. (Fragment).  
GN Name=2310015110Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RX MEDLINE=21083660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;  
RA The FANTOM Consortium;  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Tongue;

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RX MEDLINE=20499374; PubMed=11042159;
RA Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [51]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RX MEDLINE=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carinci P.,
RA Kono H., Akiyama J., Nishi K., Kitsuai T., Taisho H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi K.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Tongue;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carinci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Kono H., Koda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Nunazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi P., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK009361; BAC25254.1;
DR MGD; MG1:1916800; 2310015110Rik.
KW Hypothetical protein.
FT NON_TER 1
SQ
SEQUENCE 108 AA; 12173 MW; COEADFP2B4117889D CRC64;

Query Match 19.0%; Score 162.5; DB 2; Length 108;
Best Local Similarity 36.5%; Pred. No. 3.2e-05;
Matches 42; Conservative 19; Mismatches 33; Indels 21; Gaps 4;

QY 62 ECGNTHLLQOELTEKQKGFQVDEAQAATCNHTVMALMSLDEKQG---QKVEELG 118
DB 3 ECGNTHLLQOELTEKQKGFQVDEAQAATCNHTVMALMSLDEKQKTEAL----- 62

QY 119 EITLHKLQDASAEYERLRRENOVS-VRADKKYPPSSQSSAAAPQLITLV 172
DB 63 EITLHKLQDASAEYERLRRENOVS-VRADKKYPPSSQSSAAAPQLITLV 100

RESULT 7
Q9YMP5 PRELIMINARY; PRT; 778 AA.
AC Q9YMP5;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ldort-82 peptide.
OS Lymantiria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10449;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99124765; PubMed=9887315;
RA Kuzio J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T.,
RA Slavicek J.M., Rohmann G.F.;
RT "Sequence and analysis of the genome of a baculovirus pathogenic for
RT Lymantiria dispar.";

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RL Virology 253:17-34(1999).
DR EMBL; AF081810; AAC70268.1;
DR PIR; T30430; T30430.
DR InterPro; IPR009615; Desmo_N.
DR InterPro; IPR010989; t-snare.
DR Pfam; PF06771; Desmo_N_1.
SQ SEQUENCE 778 AA; 87841 MW; 811B8BD172CE9E43 CRC64;

Query Match 13.0%; Score 111; DB 2; Length 778;
Best Local Similarity 32.5%; Pred. No. 2.8;
Matches 38; Conservative 22; Mismatches 47; Indels 10; Gaps 4;

QY 46 IKANSEACRDGIRAMECR-VWTHLLQOELTEKQKGFQVDEAQAATCNHTVMALMSLDA 104
DB 520 LKQSELNRD-LQKAEAGDANRLOAEIIDLKRA---ASDADALNRVAQLAEAEAS 574

QY 105 EKAOQKVEELIEGHTTLNHLQDASAEYERLRRENOVSVRADKKYPPSSQSS 161
DB 575 GAADLQNRIRARLEASSGTLRLOESAAEVIALRDKEDLERRTAAS---AADQVS 627

RESULT 8
Q9K6X4 PRELIMINARY; PRT; 461 AA.
AC Q9K6X4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cell wall-binding protein.
GN Name=BH3600;
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogatawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RT Nucleic Acids Res. 28:4317-4331(2000).
RL EMBL; AP001519; BAB07319.1;
DR PIR; H84099; H84099.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M23B.
DR InterPro; IPR009061; Putativ_DNA_Bind.
DR InterPro; IPR011054; Rudmt_hyb_motif.
DR Pfam; PF01551; Peptidase_M23; 1.
SQ SEQUENCE 461 AA; 50372 MW; 2918480CD67AF3F CRC64;

Query Match 12.6%; Score 107.5; DB 2; Length 461;
Best Local Similarity 26.1%; Pred. No. 3;
Matches 31; Conservative 28; Mismatches 55; Indels 5; Gaps 2;

QY 33 ITVILGVPLIFTIRANSACRDGIRAMECR-VWTHLLQOELTEKQKGFQVDEAQAATCN 92
DB 5 ISLVAAAGLITTSILFSOSIEDA-KANSLQNOISDVQKQKQKQKTEAL----- 59

QY 93 HTVMALMSLDEKQKQKQKVEELIEGHTTLNHLQDASAEYERLRRENOVSVRADK 151
DB 60 KEVEKELGDTAEIRLDEKVEETSGKIQEKREIEVQAEIIEBKQIIEIRIAER 118

RESULT 9
Q9KA43 PRELIMINARY; PRT; 143 AA.
AC Q9KA43;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

```



DE Flagellar protein required for flagellar formation.  
GN Name=flg;  
OS Bacillus halodurans.  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
OX NCBI\_TaxID=8665;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C-125;  
RA MEDLINE=20512582; PubMed=11058132;  
RA Takami H., Nakasone K., Takaki Y., Ogasawara N., Kuhara S.,  
RA Fuji F., Hirata C., Nakamura Y.,  
RA Horikoshi K.;  
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
RL Nucleic Acids Res. 28:4317-4331 (2000).  
DR EMBL, AP001515; BAB06166.1; --  
DR PIR, G83955; G83955.  
DR GO; GO:0009425; C:Flagellar basal body (sensu Bacteria); IEA.  
DR GO; GO:0006935; P:chemotaxis; IEA.  
DR GO; GO:0001539; P:ciliary/flagellar motility; IEA.  
DR InterPro; IPR005503; FILF.  
DR Pfam; PF03748; FILF; 1.  
KW Flagellum.  
SQ SEQUENCE 143 AA; 16386 MW; 613446D64B1C5402 CRC64;  
Query Match 12.5%; Score 107; DB 2; Length 143;  
Best Local Similarity 22.1%; Pred. No. 0.99; Mismatches 49; Indels 26; Gaps 4;  
Matches 31; Conservative 34; Mismatches 49; Indels 26; Gaps 4;  
QY 23 LGGIGIVLVIIIVLIPVLIIFTIKANSEACRDLGRAVMEC-----RNVTHLLOQL 74  
DB 6 LVNIMLITLIVTLVGVAVLIFVNYENNEDEQDRPTIDEIQAQSYETREITLNLSDNF 65  
QY 75 TEA-----QKGVQVBAQAATCNHTYVMAASLDAEKAQGGKVELESEITTLNKK 126  
DB 66 VRAEFLHVDRNMAQVQKRFQVNNIIRSLAGDMSQSLGADIGKLEAQ----- 118  
QY 127 LODASAEVRLRENOVLSV 146  
DB 119 LQD---DINALMQEGSVVKI 135  
RESULT 10  
Q7ZTT2 PRELIMINARY; PRT; 560 AA.  
ID Q7ZTT2; PRT; 560 AA.  
AC Q7ZTT2;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Similar to K1A1536 protein.  
GN Name=zgc:56638;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RA MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,  
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=whole body;  
RA Strausberg R.;  
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL, BC051625; AAH51625.1; --  
DR InterPro; IPR02017; Spectrin.  
SQ SEQUENCE 560 AA; 64730 MW; 331CDB35CB9DDB8E CRC64;  
Query Match 12.2%; Score 104.5; DB 2; Length 560;  
Best Local Similarity 26.0%; Pred. No. 6.4;  
Matches 27; Conservative 30; Mismatches 40; Indels 7; Gaps 2;  
QY 51 EACRDLGRAVME--CRNVTHLLOQLTEAOKGFQVBAQAATCNHTYVMAASLDAEKAQ 108  
DB 185 EILRSDMSQIEQLNTLIR-----STKTELEKHKKEAQSSSSMSAEFNALLAERAE 239  
QY 109 GOKVLELESEITTLNKKLODASAEVRLRENOVLSVRIADKK 152  
DB 240 NQQRKELEQDSATLTQOKQDIKALEFKRKVRKMTIQRDER 263  
RESULT 11  
HCR\_PANPA STANDARD; PRT; 782 AA.  
AC 08H57;  
DT 29-MAR-2004 (Rel. 43, Created)  
DT 29-MAR-2004 (Rel. 43, Last sequence update)  
DT 05-JUN-2004 (Rel. 44, Last annotation update)  
DE Alpha helical coiled-coil rod protein.  
GN Name=HCR;  
OS Pan paniscus (Pygmy chimpanzee) (Bonobo).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
OX NCBI\_TaxID=9597;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Aasmalahti K., Kere J.;  
RT "HCR gene orthologs in chimpanzee, pygmy chimpanzee, gorilla, and  
RT orangutan.";  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May be a regulator of keratinocyte proliferation or  
CC differentiation (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear and cytoplasmic (By similarity).  
CC -----  
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CC -----  
CC EMBL, AY135831; AAN12282.1; --  
CC EMBL, AY135815; AAN12282.1; JOINED.  
CC EMBL, AY135816; AAN12282.1; JOINED.  
CC EMBL, AY135817; AAN12282.1; JOINED.  
CC EMBL, AY135818; AAN12282.1; JOINED.  
CC EMBL, AY135819; AAN12282.1; JOINED.  
CC EMBL, AY135820; AAN12282.1; JOINED.  
CC EMBL, AY135821; AAN12282.1; JOINED.  
CC EMBL, AY135822; AAN12282.1; JOINED.  
CC EMBL, AY135823; AAN12282.1; JOINED.  
CC EMBL, AY135824; AAN12282.1; JOINED.  
CC EMBL, AY135825; AAN12282.1; JOINED.  
CC EMBL, AY135826; AAN12282.1; JOINED.

DR EMBL; AY135827; AANI2282.1; JOINED.  
 DR EMBL; AY135828; AANI2282.1; JOINED.  
 DR EMBL; AY135829; AANI2282.1; JOINED.  
 DR EMBL; AY135830; AANI2282.1; JOINED.  
 DR InterPro; IPR009800; HCR.  
 DR Pfam; PF07111; HCR; 1.  
 DR Coiled coil; Differentiation; Nuclear protein.  
 KW DOMAIN 82 314 Coiled coil (potential).  
 FT DOMAIN 344 437 Coiled coil (potential).  
 FT DOMAIN 498 691 Coiled coil (potential).  
 SQ SEQUENCE 782 AA; 88688 MW; 6F07A52DA6741377 CRC64;  
 Query Match 12.2%; Score 104.5; DB 1; Length 782;  
 Best Local Similarity 25.3%; Pred. No. 9;  
 Matches 39; Conservative 32; Mismatches 44; Indels 39; Gaps 7;  
 QY 54 RDGLRAVME-----CRNYTHL---QDELTEAKGFQDVEAQ-AATC-----NHTYMA 97  
 DB 284 RSLQATVELLQVRVQSLTHIALQEEELTRKVPDSLEPFTRKQSLNRMREKVFYA 343  
 QY 98 LMASLDAEKAQCKKVEBELGETTITLNNK-----LQDASAEVERLRRENGV 143  
 DB 344 LNVQLKAQELHSDSVKQLKGVAQLQKVTSGSQEQAILQSLQDKAAEVERMGANG 403  
 QY 144 LSVRI-----ADKKYPPSSQDSSSAAPQLITVL 172  
 DB 404 LQLELSRAQEARRRW-----QQQTASAEQRLIV 433

RESULT 12  
 HCR PANTR STANDARD; PRT; 782 AA.  
 AC 08H2C0; Q7YR47;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Alpha helical coiled-coil rod protein.  
 GN Name:HCR;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Asunahatci K., Kere J.;  
 RT "HCR gene orthologs in chimpanzee, pygmy chimpanzee, gorilla, and  
 RT orangutan."  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;  
 RA Anzai T., Shlita T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,  
 RA Yamagata T., Kuletski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,  
 RA Yamazaki M., Tashiro H., Iwamoto C., Uemehara Y., Imanishi T.,  
 RA Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;  
 RT "Comparative sequencing of human and chimpanzee MHC class I regions  
 RT unveils insertions/deletions as the major path to genomic  
 RT divergence";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).  
 CC - FUNCTION: May be a regulator of keratinocyte proliferation or  
 CC differentiation (by similarity).  
 CC - SUBCELLULAR LOCATION: Nuclear and cytoplasmic (by similarity).  
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DR EMBL; AY135777; AANI2279.1; -  
 DR EMBL; AY135761; AANI2279.1; JOINED.

DR EMBL; AY135762; AANI2279.1; JOINED.  
 DR EMBL; AY135763; AANI2279.1; JOINED.  
 DR EMBL; AY135764; AANI2279.1; JOINED.  
 DR EMBL; AY135765; AANI2279.1; JOINED.  
 DR EMBL; AY135766; AANI2279.1; JOINED.  
 DR EMBL; AY135767; AANI2279.1; JOINED.  
 DR EMBL; AY135768; AANI2279.1; JOINED.  
 DR EMBL; AY135769; AANI2279.1; JOINED.  
 DR EMBL; AY135770; AANI2279.1; JOINED.  
 DR EMBL; AY135771; AANI2279.1; JOINED.  
 DR EMBL; AY135772; AANI2279.1; JOINED.  
 DR EMBL; AY135773; AANI2279.1; JOINED.  
 DR EMBL; AY135774; AANI2279.1; JOINED.  
 DR EMBL; AY135775; AANI2279.1; JOINED.  
 DR EMBL; AY135776; AANI2279.1; JOINED.  
 DR EMBL; AB100083; BAC78167.1; ALT\_INIT.  
 DR InterPro; IPR009800; HCR.  
 DR Pfam; PF07111; HCR; 1.  
 DR Coiled coil; Differentiation; Nuclear protein.  
 KW DOMAIN 82 314 Coiled coil (potential).  
 FT DOMAIN 344 437 Coiled coil (potential).  
 FT DOMAIN 498 691 Coiled coil (potential).  
 FT DOMAIN 288 288 Coiled coil (potential).  
 FT CONFLICT 319 319 O -> H (in Ref. 2).  
 FT CONFLICT 319 319 S -> T (in Ref. 2).  
 FT CONFLICT 638 638 R -> H (in Ref. 2).  
 FT CONFLICT 671 671 R -> Q (in Ref. 2).  
 SQ SEQUENCE 782 AA; 88660 MW; D140F8587129D054 CRC64;  
 Query Match 12.2%; Score 104.5; DB 1; Length 782;  
 Best Local Similarity 25.3%; Pred. No. 9;  
 Matches 39; Conservative 32; Mismatches 44; Indels 39; Gaps 7;  
 QY 54 RDGLRAVME-----CRNYTHL---QDELTEAKGFQDVEAQ-AATC-----NHTYMA 97  
 DB 284 RSLQATVELLQVRVQSLTHIALQEEELTRKVPDSLEPFTRKQSLNRMREKVFYA 343  
 QY 98 LMASLDAEKAQCKKVEBELGETTITLNNK-----LQDASAEVERLRRENGV 143  
 DB 344 LNVQLKAQELHSDSVKQLKGVAQLQKVTSGSQEQAILQSLQDKAAEVERMGANG 403  
 QY 144 LSVRI-----ADKKYPPSSQDSSSAAPQLITVL 172  
 DB 404 LQLELSRAQEARRRW-----QQQTASAEQRLIV 433

RESULT 13  
 Q7R6H3 PRELIMINARY; PRT; 900 AA.  
 AC Q7R6H3;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE GIP 170.182668.185370.  
 GN Giardia lamblia ATCC 50803.  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=184922;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WB C6;  
 RA Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D.,  
 RA Olsen G.J., Sogin M.L.;  
 RT "Draft sequence of the Giardia lamblia genome."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 CC - CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC EMBL; AACB0100001; EAA43024.1; -  
 DR InterPro; IPR000276; GPCR\_Rhodopsin.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; UNKNOWN 1.  
 SQ SEQUENCE 900 AA; 103880 MW; 72339FBCACCA19 CRC64;  
 Query Match 12.2%; Score 104; DB 2; Length 900;  
 Best Local Similarity 30.7%; Pred. No. 11;

|                       |        |               |       |             |
|-----------------------|--------|---------------|-------|-------------|
| Query Match           | 12.1%; | Score 103;    | DB 1; | Length 782; |
| Best Local Similarity | 25.3%; | Pred. No. 12; |       |             |

Search completed: December 29, 2004, 11:43:38  
Job time : 107 secs

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